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December 28, 2000, 09:56:08; Search time 2435.54 Seconds (without alignments) 3929.054 Million cell updates/sec
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2191
1 GCCAGGACCTCTGTGAACCG......TTTTGGTACTTAAAAATGGC 2191
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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em_htg23:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AR062119 Sequence	AF053713 Mus muscu	AF019048 Mus muscu	AF013170 Mus muscu	AB022039 Mus muscu	AF053712 Homo sapi	AF019047 Homo sapi	AF013171 Homo sapi	AB008426 Mus muscu	AB036798 Mus muscu	AB032771 Mus muscu	AL139382 Homo sapi
	ID	AR062119	AF053713	AF019048	AF013170	AB022036S4	AF053712	AF019047	AF013171	AB008426	AB036798	AB032771	AL139382
	DB	ß	12	12	12	12	11	11	11	12	12	12	85
	Query Match Length DB	2295	2299	2225	2237	2029	2271	2201	1823	951	951	864	205139
*P	Query	97.9	97.9	97.8	93.2	66.7	51.1	9.09	43.7	43.4	43.4	37.3	35.2
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	2.9 256172 2.9 13859 31 2.8 160301 2.8 160301 2.8 180340 2.8 18134 2.8 85779 34 2.8 159250	2.8 151922 66 2.8 176525 65 2.7 167810 10 2.7 234112 35 2.7 234112 35 2.7 234112 35 2.7 234113 31 2.7 12813 31 2.7 157016 70		AR062119 2295 bp DNA Sequence 6 from patent US 5843678. AR062119 AR062119.1 GI:5989810 Unknown.	<pre>f Unknown. Unclassified. 1 (bases 1 to 2295) BOYle,W.J. Osteoprotegerin binding proteins Patent: US 5843678-A 6 01-DEC-1998; Location/Qualifiers 1 2296</pre>	/organism="unknovn" 648 a 487 c 538 g 622	Ouery Match 97.9%; Scole 2144.8; DB 5; Length 2295; Best Local Similarity 99.4%; Preć. No. 0; 0; Nismatches 12; Indels 2; G Matches 2174; Conservative 0; Nismatches 12; Indels 2; G 1 GCAGGACTCTGTGAACGGTGGGGG GGGGCCCCCTGCCGGGAGTTGCTGCTGCGGG 111111111111111111111111111111111111	

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2299 bp mRNA osteoprotegerin ligand

GI:3057147

AF053713 2 Mus musculus c AF053713 AF053713.1 G1

LOCUS DEFINITION ACCESSION VERSION

KEYWORDS

AF053713 .

RESULT

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1 (bases I to 2299)
Lacey,D.L. Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,
Delaney,J. and Boyle,W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
Cell 93 (2), 165-176 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="osteoprotegerin ligand"
/product="asteoprotegerin ligand"
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/db_xref="6[1:3057148"
/db_xref="6[1:3057148"
/translation="mkrashDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPPA
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APFAHLTINAASIPSGSHKVLLSSWYHDRGWARISNMTLSNGKLRVNQDGFYLYAN
IGCRRHHFTSGSVPTDYLQLMYYVWTSIRIPSSHNLMKGGSTKNWSGNSEFHFYSINV
GGFFKLRAGEBISIQVSNPSLLDPDQDATYFGAFKVQDID"
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   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Involve Amgen Center Drive, Thousand Oaks, California 91320, USA

Location/Qualifiers
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Mammalia; Eutheria; Rodentia;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2225)
Anderson, D. M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C., Tometsko, M.E., Roux, E.R., Teepe, M.C., Dubose, R.F., Cosman, D. and 22-NOV-1997 factor kappa B ligand 1800 1860 1920 1980 2040 1844 2083 2143 2023 1545 GGGACCTGCAAATAAGTTCTTTTTTTTTAATGAGGAGAGAAAAATATATGTATTTTTTATA 1604 2144 ATCCACTTTTTAATTTAGTGAAAGTTATTTATTATATACTGTACAATAAAAGCATTGTCTC 2203 Galibert, L.
A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function
Nature 390 (6655), 175-179 (1997) 51 1665 TTGTGCTATAGTATTTGATTCAAAATATTTAAAAATGTCTCACTGTTGACATATTTAATG TITIAAAIGIACAGAIGIATIIAACIGGIGCACIIIIGIAAIICCCCIGAAGGIACICGIA GCTAAGGGGGCAGAATACTGTTTCTGGTGACCACATGTAGTTTATTTCTTTTTT AAATGAATATCTTGAATAATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAATTTAGAA 1905 AAATGAATACCTTGAATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAATTTAGAA GCTAATTGACTTTAGGAGCTGACATAGCCAAAAAGGATACATAATAGGCTACTGAAAATC 1965 GCTAATTGACTTTAGGAGCTGACATAGCCAAAAAGGATACATAATAGGCTACTG-AAATC Anderson, D. M. Billingsley, W., Dougall, W., Maraskovsky, E., Cosman, D., DuBose, R. and Galibert, L. Direct Submission
Submitted (13-40G-1997) Molecular Biology, Immunex Corp., University St., Seattle, WA 98101, USA TTGTGCTATAGTATTTGATTCAAAATATTTAAAAATGTCTCACTGTTGACATATTTAATG 2041 TAAATTTTGTTTTTTTTTCCCATAGAAAATGTACTATAGTTTATCAGCCAAAAACA 2101 ATCCACTTTTAATTTAGTGAAAGTTATTTTATTATACTGTACAATAAAAGCATTGTTTC TAATGTCTAAAGTTATATTTCAGGTGTAATGTTTTCTGTGCAAAGTTTTGTAAATTATAT AF019048 2225 bp mRNA ROD Mus musculus receptor activator of nuclear i (RANKL) mRNA, complete cds.
AF019048.1 GI:2612923 2161 TGAATGGCATTTTTTGGTACTTAAAAAT 2188 (bases 1 to 2225) house mouse. Mus musculus RESULT 3
AF019048
LOCUS
DEFINITION ORGANISM 1561 1605 1621 1741 1921 1681 1725 1861 2204 JOURNAL MEDLINE TITLE JOURNAL ACCESSION REFERENCE VERSION KEYWORDS SOURCE AUTHORS REFERENCE AUTHORS TITLE g ò οy qq ò QQ ò Ob ò Db ò q ò QQ ò qq q ò g ò g à

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ICFRHHETSGSVPPTVLQLWYVYKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINV
GGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID"
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Location/Qualifiers
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Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 2237)
Wong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M.,
Kalachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y.
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                              AAATGAATATCTTGAATAATAAGTAGGAMGTTGGTCACCAGGTGCCTTTCAAATTTAGAA 1920
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1752 GCTAAGGGGGCAGAATACTGTTTCTGGT/HACCACATGTAGTTTATTTCTTTATTCTTTTT 1811
                                             1812 AACTTAATAGAGTCTTCAGACTTGTCAANACTATGCAAGCAAAATAAATAAATAAAAATA 1871
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells J. Biol. Chem. 272 (40), 5190-25194 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANCE (tumor necrosis factor [TNF]-related activation-induced cytokine), a new TNF family member predominantly expressed in feells, is a dendritic cell specific survival factor J. Exp. Med. 186 (12), 2075-2080 (1997)
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Fuller,K., Wong,B.; Fox,S., Choi,Y. and Chambers,T.J.
TRANCE is necessary and sufficient for osteoblast-mediated
activation of bone resorphion in osteoclasts
J. Exp. Med. 188 (5), 997·1001 (1998)
                                                                                                                                                                                                                                                                   TGTCAGGAGTATTATGCAATTATTGAA.AGGTGTCTTTTTTACAAGAGCTACAAATTG
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Mus musculus TNF-related ligand TRANCE mRNA,
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J. Biol. Chem. 273 (43), :8355-28359 (1998)
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AQPFRHLTINAASIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYAN
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                    Hughes Med
ork Ave., 1
                                                                                                                                     /map="near Rb1"
/cell_line="T cell hybridoma
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Pred. No. 0;
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                                                                                                                                                                                       /note="TNF-related ligand'
Direct Submission
Submitted (09-JUL-1997) Howard Hug
Rockefeller University, 1230 York
                                                                                    /organism="Mus musculus
                                                                                                    /db_xref="taxon:10090"
/chromosome="14"
                                                   Location/Qualifiers
                                                                                                                                                                                                                         /product="TRANCE"
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Best Local Similarity 98.4%;
Matches 2155; Conservative (
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661 TAAAGTCACTCTGTCCTCTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGAC 720	GTATCTCGTTAAAACCAGCACCAAATCCCAAGTTCTCATAACCTGATGAAGGGGGGGG	TTTCAAGCTCCGAGCTGGTGAAGAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGA 	1081 ATTICGTGGAACATTAGCATGGTCCTAGATGTTTGGAAACTTCTTAAAAAATGGATG 1140	01 CCTCTCTTGAG-CCTGTACAGGTTGTATATGTAAGGTCCATAGGTGTTAGATT 1	1320 TGGGAAGGTATTCCGATGCTTATGAAAACTTACACGTGAGCTATGGAAGGGGTCACA 1379	1397 GTCTCT-GGTCTAACCCCTGGACATGTGCCACTGAAACCTTGAAATTAAGAGGATGCCA 1455 1440 TGTCATTGCAAAGAAATGATAGTGTGAAGGGTTAAGTTCTTTTGAATTGTACATTGCC 1499	1560 ATAATGTCTAAAGTTATATTTCAGGTGTAATGTTTTCTGCCAAAGTTTTGTAAATTATA 1619 	1620 TTTGTCCTATAGTATTGATTCAAAATATTAAAAATGTCTCACTGTGACATATTTAAT 1679 1634 TTTGTCCTATAGTATTGATTCAAAATATTAAAAATGTCTCACTCTTGACATATTTAAT 1693 1680 GTTTTAAATGTACAGATGTATTTAACTGGTGCACTTTGTAATTCCCTGAAGGTACTCGT 1739 11694 GTTTTAAATGTACAGATGTATTTAACTGGTGCACTTTGTAATTCCCCTGAAGGTACTCGT 1739 11694 GTTTTAAATGTACAGATGTATTTAACTGGTGCACTTTGTAATTCCCCTGAAGGTACTCGT 1753
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aira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N.,
akami,A., Ueda,M. and Higashio,K.
ning and characterization of the gene encoding mouse osteoclast
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SAATATCTTGAATAATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAATTTAGA 1919
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sect Submission
ect Submission
mitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases.
ihiko Kodaira, YS New Technology Institute Inc., Molecular
logy: Shimoishibashi 519, Ishibashi-machi, Tochigi 329-0512,
an (E-mail:YSNT@t-cnet.or.jp, Tel:81-285-52-2821,
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join(AB022036.1:409. .630,AB022037.1:169. .330,
AB022038.1:146. .182,AB022038.1:274. .372,159. .580)
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/protein_id="BAA36970.1"
/db_xref="G1:4127270"
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/strain="129"
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STLESEDTLPDSCRRWK(AFQQAVQKRLQHIVGPQRFSAMMEGSWLDYAQRGKPEAQP
STALTINABAIPSGSHKYYLSSWYHDMAKISHWILSNGKLRVNQDGFYYLYANICF
RHHETGSQPFDYYLQLMYYVYKTSIKIPSSHYLMKGGSTKNWSGNSEFHFYSINVGGF
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Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R., Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S., Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A. Olan, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo Osteoprotegarin ligand is a cytokine that regulates osteoclast differentiation and activation
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Submitted (16-MR-1998) Department of Cell Biology, Amgen, Inc., 2014 Coetion Qualifiers and oaks, California 91320, UsA 1.02211 Coetion Qualifiers and oaks, California 91320, UsA 1.02211 Coetion Qualifiers osteoclast differentiation and activation." regulates osteoclast differentiation and activation." regulates osteoclast differentiation and activation." regulates osteoclast differentiation and activation." 138 // Month	658 a 658 a 659; conscient in it in
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/db_xref="G1:2612022"
/translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAA
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Anderson, D.M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C.
Tometsko, M.E., Roux, E.R., Teepe, M.C., DuBose, R.F., Cosman, D.
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Anderson, D.M., Billingsley, W., Dougall, W., Maraskov Cosman, D., DuBose, R. and Gilibert, L.
Subricet Submission
Submitted (13-AuG-1997) Molecular Biology, Immunex University St., Seattle, W., 98101, USA
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                                              AGGITGTGTATATGTAAAGTCCA-TAGGTGATGTTAGATTCATGGTG-ATTACACAACGG
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RRIKQAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHTINATD
IPSGSHKVSLSSWYHDRGWKISNMFFSNGKLIVNQDGFYYLVANICFRHHETSGDLA
TEYLQLMYVYTKTSIKIPSSHTLMKGSSTKYWSGNSEFHFYSINVGGFFKLRSGEEIS
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305 c 380 g 569 t
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1 (bases 1 to 1823)
Rong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M., Ralachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y. and Choi, Y.
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2 /400122
2 /60ses 1 to 1823)
Wong, B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
Direct Submission
Submitted (09-JUL-1997) Howard Hughes Medical Institue, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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Homo sapiens TNF-related Ligand TRANCE mRNA, partial cds.
AF013171
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domain"
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/note="encodes extracellular
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/db_xref="G1:2411500"
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/db_xref="taxon:9606"
/chromosome="13"
/map="13q14"
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Db 11	Qy 153 Db 117	Oy 159 Db 123	Qy 169 Db 129	Qy 173 Db 135	Qy 176 Db 141	Oy 187 Db 147	Oy 186 Db 152	Oy 194 Db 156	Qy 200 Db 163	Qy 206		Oy 216 Db 181	RESULT AB008426 LOCUS	DEFINITA ACCESSIC VERSION	KEYWORDS SOURCE ORGANI	REFERENC AUTHOR	TITLE JOURN	REFERENC
	2	518 CACATTGTGGGGCCACAGCGCTTCTCAGG AGCTCCAGCTATGATGGAAGGCTCATGGTTG 577 	578 GATGTGGCCCAGCGAGGCAGCCTGAGGCCCATTTGCACACCTCACCATCAATGCT 637 	638 GCCAGCATCCCATCGGGTTCCCATAAAGICACTCTGTCTTGGTACCACGATCGAGGC 697		758 TTCTATTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCT 817 	818 ACAGACTATCTTCAGCTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGTTCT 877 	878 CATAACCTGATGAAGGGGGGGGGCAGCAAAACTGGGGCAATTCTGAATTCCACTTT 937 	938 TATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGGCTGGTGAAGAAATTAGCATTCAG 997 	998 GTGTCCAACCCTTCCCTGCTGGATCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAA 1057 	1058 GTTCAGGACATAGACTGAGACTCATTTCG FGGAACATTAGCATGGATGTCTTAGATGTTT 1117 	1118 GGAAACTTCTTAAAAAATGGAT3ATGTCTATACATGTGTAAGACTACTAAGAG 1170 	1171 ACATGGCCCACGGTGTATGAAACTCACAGGCCTCTCTTGAGCCTGTACAGGTTGTGTA 1230 	1231 TATGTAAAGTCCATAGGTGATGTTAGAGTG-ATTACACAACGGTTTTACAATTT 1289 	290 TGTAATGATTTCCTAAGAATTGAACCAGA FTGGGAGGGGGTTTCCGATGCTTATGAAAAA 1349 	1350 CTTACACGTGAGCTATGGAAGGGGTCACAGTCTCTGGGTCTAACCCCTGGACATGTGCC	1410 ACTGAGAACCTTGAAATTAAGAAGATGCC YTGTCATTGCAAAGAAATGATAGTGTGAAGG 1469 	1470 GTTAAGTTCTTTGAATTGTTACATTGCG TGGGACCTGCAAATAAGTTCTTTTTTCTA 1529
QQ	Qy Db	Qy Db	Qy	Qy Dp	Qy Db	Qy Dp	Qy	Qy Db	Oy Db	Qy Dp	Oy 1	Oy 1 Db	Qy 1 Db	Oy 1 Db	Oy 1	0y 1:	Qy 1,	0y 1

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Mus musculus bone marrow stromai cells cell_line:ST2 cDNA to mRNA, clone_lib:pcDL-SRa296 clone:pOBM291.

Mus musculus
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 951)
Yasuda,H.
                                                  004 TIGAACAGGIGICITITITIACAAGAGCIACAAAITGIAAAITITIGITITITITITICC
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                                  ATGAGGAGAGAAAATATATATTTTTATAAATGTCTAAAGTTATATTTCAGGTGTAA
                                                                                                                                                                            TAAAAATGTCTCACTGTTGACATATTTAATGTTTTAAATGTACAGATGTATTTAACTGGT
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$AB008426.1 GI:3041781 osteoclast differentiation factor (ODF)
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Mus musculus mRNA
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Yasuda,H., Shima,N., Nakagawa,N., Yamaguchi,K., Kinosaki,M., Mochizuki,S., Tomoyasu,A., Yano,K., Gotc,M., Murakami,A., Tsuda,E., Morinaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T. Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is
                                                                                                                                                                                                                                                                                                                                                                STLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPE
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267 c 248 g 205 t
                                                                       identical to TRANCE/RANKL
Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)
98188248
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Pred. No. 1.4e-166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ransmenbrane domain"
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                                                                                                                                                                                                                        /clone_lib="pcDL-SRa296"
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1.951
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Matches 951; Conserv
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/translation="mrrasrdygkylksseemgsgpcyphegplappapapppa
Asrswrlaliglggyvcstaletyrrambentsedstriktlenbaglod
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Aqppahltinaasipsgswythskawtismmllskgkpe
Icrrhetsgsyptdilolmyyvvktsikipsshvlmkggsrknwsgnsefheysinv
Ggffkleragesiziqysnpslldpdodatyfgafkvqddd"
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Submitted (11-JAN-2000) to the DDBJ/EWBL/GenBank databases. Tohru
Steda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus
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                                                                         GTCACTCTGTCCTTGGTACCACGATCGAGGCTGGGCCCAAGATCTCTAACATGACGTTA
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Mus musculus mRNA for RANKL 1, complete
AB036798
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Mammalia; Eutheria; Rodentia;
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/product="RANKL 1"
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NF-kB ligand

mRNA ROD 25 mRNA for receptor activator of

864 bp RANKL 2 r

Mus musculus complete cds

LOCUS

AB032771

Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

ligand

receptor activator of NF-kB

AB032771.1 GI:8843822

AB032771

ACCESSION

VERSION KEYWORDS

Mus musculus cDNA to mRNA Mus musculus

ORGANISM

SOURCE

1 (bases 1 to 864) Ikeda,T.

AUTHORS TITLE

REFERENCE

TITLE

AUTHORS

Submitted (78-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8919, Japan (E-mail:toru.pth/@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)

/organism="Mus musculus" /db_xref="taxon:10090"

Location/Qualifiers

.864

source

FEATURES

gene

Receptor activator of NF-kB ligand 2 Published Only in DataBase (2000) In press 2 (bases 1 to 864) Ikeda.T. Direct Submission

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                         Length 951;
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                               . No. 1.4e-166;
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                       43.4%; Score 951; DB 12;
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Live 0; Mismatches 0;
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                               Similarity
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/translation="mrasroygkylrtprasrsmflallglglggvvcsialfyrra dmdprrisedsthctyrrikklhenglgdstlesedtldsdstrmkgafggavgkeld HVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWTHD RGWAK ISNWTLSNGFLRVNQDGFYYLYANICPRHHETSGSVPTDYLQLMVYVVKTSIK IPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDAT ó 213 273 333 424 484 544 604 393 304 Gaps 93 245 CCGCCACCCGCCGCCTCCGTTCCTGGCCCTCCTGGGGCTGGGACTGGGCCAG GGAGCTCCAGCTATGATGGAAGGCTCATGGTTGGATGTGGCCCAGCGAGGCAAGCCTGAG CAGGACTCGACTCTGGAGAGTGAAGACACACTACCTGACTCCTGCAGGAGGATGAAACAA GCCTTTCAGGGGCCCGTGCAGAAGGAACTGCAACATTGTGGGGGCCACAGCGCTTCTCA TCAGAAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAAACGCAGGTTTG 5 ; 0 864; NF-kB ligand Length Indels DB 12; Score 818.2; DB 12; Pred. No. 5.6e-142; 0; Mismatches 8; οŧ /product="receptor activator /protein_id="BAA97257.1" /db_xref="GI:8843823" 197 Б 219 /gene="RANKL 2" /codon_start=1 /gene="RANKL 2" 37.3%; 99.0%; YFGAFKVQDID" O 823; Conservative 1. .864 227 Similarity 221 Query Match Local BASE COUNT 365 Matches 425 485 545 274 334 CDS ORIGIN qq g qq g à ò Ω q δ Q

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Direct Submission
Submitted (05-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire,
CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 7, 2000 this sequence version replaced gi:8388479.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCTCCGAGCTGGTGAAGAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCG 1024
                                                                                             633
                                                                                                                                                                                                                                                                                                                                           693
                                                                                                                                                                                                                                                                                                                                                                                                  AL139382 205139 bp DNA HTG 06-JUL-2000 HOMO sapiens chromosome 13 clone RP11-86N24, *** SEQUENCING IN PROGRESS ***, 27 unordered pieces.
                   724
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                                                                                                                                                                                                                            TTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT 844
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Insert size: 162413; 9.2% error; agarose-fp
Quality coverage: 3.08x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGC
                                                                                                                                                                     GCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCATAAA
                                                                          GTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA
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Catarrhini; Hominidae; Homo
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Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 185877 bases at least Q40
Consensus quality: 193731 bases at least Q40
Consensus quality: 198268 bases at least Q20
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    Project Information

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
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Mammalia; Eutheria; Primates;
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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42114: gap of 100 bp
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56692: contig of 6439 bp in length
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1013 bp in length
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34870: contig of 2399 bp in length
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61250: contig of 4458 bp in length
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fragment_chain:1"
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BASE COUNT ORIGIN

17; Db 135443 CAACCCTCCTTACTGGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTTAAAGTTCG 135502 135679 DD 135843 GCAGC-TGAAGTGGAGAGGGTGTCATCT-AGCGCAATTGAAGGATCATCTGAAGGGGCAA 135900 1175 1176 GCCCACGGTGTATGAAACTCACAGCCCTCTTTGAGCCTGTACAGGTTGTGTATATGT 1235 1415 GAACCTTGAAATTAAGAAGGCATGTCATTGCAAAGAAATGATGGTGGAAGGCTTAA 1474 1003 CAACCCTTCCCTGCTGGATCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTTCA 1062 GGACATAGACTGAGACTCATTTCGTGGAACATTAGCATGGATGTCCTAGATGTTTGGAAA 1122 822 942 Gaps 943 CATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTC CTTCTTAAAAA-----ATGGATGATGTCTATACATGTGTAAGACTACTAAGAGACATG ACGTGAGCTATGGAAGGGGGTCACAGTCTCTGGGTCTAACCCCTGGACATGTGCCCACTGA DD 135958 GAGAG-AAAATATATATTTATATATATCTAAAGTTATATTTCAGATGTAATGTTT 643 CATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGC 703 CAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTA TTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCAGA CTATCTTCAGCTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGTTCTCATAA 883 CCTGATGAAAGGAGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCCACTTTTATTC 1475 GITCITITGAAITGITACAITGCGCTGGGACCTGCAAAIAAGITCITITITCIAAIGAG 1535 GAGAGAAAATATATATTTTTATATATGTCTAAAGTTATATTTCAGGTGTAATGTTT 67; Length Indels Score 771.8; DB 85; Pred. No. 2.2e-133;); Mismatches 302; ó 35.2%; 76.3%; Conservative Similarity Best Local Sim Matches 1190; Query Match 763 823 1123 1355 135203 135323 1063 q QQ g qq g g ò ò δ Qγ ò ογ δ δ ολ ò ŏ ò ò

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Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3,
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Direct Submission

Direct Submission

Submission

Submission

Submission

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Submission

Ikeda (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru

Department of Pathology and Immunology; 1-5-45 Yushina, Bunkyo-ku,

Tokyo 113-8519, Japan (E-mail:toru.pth/2@med.tmd.ac.jp,

Tel:81-3-S803-5176, Pass:81-3-S803-0123)
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Sciurognathi; Muridae; Murinae; Mus
             136077 AIGICTIGCIGITGACAIATITAAIGITTIAAAIGIACAGACAIAITIAACTGGIGCACI 136136
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                                                                                                                                                                                                                                                         136474 ATAGAAAAGTTATTAGTGGTTTATCAGCAAAAAGTCCAATTTTAATTTAGTAAATGTTĀ 136533
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ATGTCTCACTGTTGACATATTTAAATGTTTTAAATGTACAGATGTATTTAAACTGGTGCACT 1714
                                                                                                                                                                                                                                         TGTTGGTCACCAGGTGCCTTTCAAATTTAGAAGCTAATTGACTTTAG-GAGCTGACATAG 1947
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                                                          TTGTAATTCCCCTG-----AAGGTACTCGTAGCTAAGGGGGCAGAATACTGTTTCTGGTG
                                                                          Db 136137 TTGTAAAATTCCCTGGGGAAAACTTGCAGCTAAGGGGGGAAAAAAATGTTGCTAAT
                                                                                                                    ACCACATGTAGTTTTTTTTTTTTTTTTAACTTAATAGA-GTCTTCAGACTTGTCAA
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    /organism="Mus musculus"
    /db_xref="taxon:10090"
    155. .754

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Mammalia; Eutheria; Rodentia;
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Somatostatin, a new marker
of RaNKL isoforms
Unpublished (1999)
2 (bases 1 to 754)
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Mus musculus
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155. .754
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//translation="MKOAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEA
OPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANI
CFRHHETSGSVPTDYLQLMYYVVRTKIRIPSSHNLMKGGSTKNWSGNSEFHFYSINVG
GFRKHRAGEELSYOSPRSLLDPDQDATYFGAFKVQDID"
190 c 185 g 170 t
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E RP11-21H9, WORKING DRAFT SEQUENCE, 13 unordered
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                                                                                                                                                  Length 754;
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Pred. No. 6.8e-125;
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nes 726; Conservative
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in length

ORGANISM

KEYWORDS

AUTHORS TITLE

REFERENCE

REFERENCE AUTHORS

JOURNAL

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75674 75773: gap of 100 bp
75774 92375: contig of 16602 bp in length
92376 92475: gap of 100 bp
92476 113451: contig of 20976 bp in length.
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75673: contig of 12625 bp in length
         p of 100 bp
contig of $873 bp in length
p of 100 bp
contig of 5190 bp in length
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/db_xref="taxon:9606"
/clone="RP11-21H9"
/clone_lib="RPCI-11 Human Male BAC"
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f 7485 bp
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/note="assembly_fragment"
/ 11042 c 23371 g 31675 t
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17436. .23308

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23409. .28598

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/note="assembly_fragment
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                                                                                                                                                                                                                         Shring Birnen B., Linton L., Nusbeum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Berna, N., Beda, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Berna, N., Beda, F., Boguslavkiy, L., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Castle, A., Cohepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewark, K., DeGe, S., Domino, M., Doyle, M., Fenestor, J., Erreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Lant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Largcque, K., Lehocaky, J., Levine, R., McGark, A., McKernan, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Medrim, J., Marova, T., Miranda, C., Menga, V., Morrow, J., Naylor, J., Peterson, K., Pierre, N., Pierre, N., Pierre, N., Pierre, N., Pierre, N., Pierre, N., Paland, C., Pollara, V., Raymond, C., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tirrall, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Nod., M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Mar 3, 2000 this sequence version replaced gi:7139552. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 113451)
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Center code: WIBR
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Insert size: 112251; sun-of-contigs
Quality coverage: 3.5 in 020 bases; agarose-fp
Quality coverage: 4.3 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L4020
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                                                                                                                                        Birren, B., Linton, L., Nusbeum, C. and Lander, E. Homo, sapiens, clone RP11-21H9
4TG; HTGS_PHASE1; HTGS_DRAFT.
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                                              Homo sapiens
                                                                                                                                                                                       Unpublished
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TITLE JOURNAL

COMMENT

12; 643 CATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTTTGGTACCACGATCGAGGCTGGGC 702 Gaps 703 CAAGATCTCTAACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTA 763 TTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGA DB 77; Length 113451; 54; 1200 others Indels 31.4%; Score 688.4; DB 77; 71.8%; Pred. No. 6.3e-118; tive 0; Mismatches 341;

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11874 ATTCTTTTGAATTGTTACATCATGCTGGAACCTGCAAAAATAC---TTTTTCTAATGAG 11818
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EYLQLMYYUTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Masazumi Nagai, Iwate Medical University School of Dentistry, Department of Biochemistry; 19-1 Uchimaru, Morioka, Iwate 020-8505, Japan (E-mail:mnagan@ilwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436), Fax:+81-19-654-4147)
Craniata; Vertebrata; Euteleostomi;
                                                                                                    mRNA
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Cancer cells responsible for humoral hypercalcemia express mRNA
encoding a secreted form of ODF/TRANCE that induces osteoclast
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Direct Submission
Submitted (26-JAN-2000) to the DDBJ/EMBL/GenBank databases
                                                                    CAAAAAGGATACATAATAGGCTACTGAAAATCTGTCAGGAGTATTTATGCAATTATTGAA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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/db_xref="taxon:9606"
/cell_line="SCC-4"
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/db_xref="G1:6863048"
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Homo saptiens
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Primer used to amp Mouse apoptosis in Murine TRAIL polyp Murine AGP-1 encod INF-related apopto P. falciparum Proj Plasmodium Proj3 g

P. falciparum

Human TL2 cDNA.

Human tumour necro TNF-related apopto Novel cytokine Apo

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Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis; antagonist; autoimmune disorder; rheumatoid arthritis; systemic lupus erythematosus; Hashlmoto's autoimmune thyroiditis; acute inflammatory response; antibody; antigen; cancer; ss.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Score

Result No. ~

P-PSDB;

treat conditions ე Surface antigen, 49969 process with abnormal physiology or development Mouse cell associated

Claim 4; Pages 8-11; 59pp; Englis 1.

abnormal physiology or development. The 4999 protein is expressed highly on polarised ThI T cells, binding of 4999 protein is expressed highly on polarised ThI T cells, binding of 4999 protein is expressed highly on polarised ThI T cells, binding of 4999 protein is expensed to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's rutoimmune thyroiditis, as well as acute inflammatory responses in which T-cell expansion, activation or immunological T-cell memory play in important role. The antibodies can be used to raise anti-idiotype antibodies which will be useful to the expression of antigens of 4999. The antibodies, and fragments of 4999 can be used in the treatmen: of conditions associated with abnormal physiology or development, including abnormal proliferation (e.g. cancerous conditions) or developmentive conditions. is is the nucleotide sequence encoding the mouse 499E9 protein, the method of the invention to treat conditions associated with in

Sequence 2191 BP; 605 A; 461 C; 5:8 G; 607 T; 0 other;

0 Gaps 2191; ; DB 19; Length Indels ö 0; M.smatches 100.0%; Score 2191; 100.0%; Pred No. 0;

120 240 180 240 TGGGTGGCCGAGGAAGGAAGAACGATJGCGGAGCAGGGCGCCCGAACTCCGGGCGCCC 120 CGCCATGCGCCGGGCCAGCCTAC GCAAGTACCTGCGCAGCTCGGAGGAGATGGG 180 300 300 360 420 420 480 540 540 009 900 9 9 GCCAGGACCTCTGTGAACCGGTCGGGGC\GGGGCCGCCTGGCCGGGAGTCTGCTCGGCGG cageggeeceggegteecacaegagggtuegetgeaeceggegeettetgeaeeggetee tgggtggccgaggaagggagagacgat. gcggagcagggcgcccgaactccggggcgccg CAGCGGCCCCGGCGTCCCACACGAGGGT\CGCTGCACCCCGCGCCTTCTGCACCGGCTCC GGCGCCCCCCCCCCCCCCCCCCCCCATGTTCCTGGCCCTCCTGGGGCTGGGACTGGG CCAGGTGGTCTGCAGCATCGTTCCTTTTCCATCGCAGCGCAGATGGATCCTAACAG ccaggtggtctgcagcatcgctctgttcvtgtactttcgagcgcagatggatcctaacag TTTGCAGGACTCGACTCTGGAGGGGAA;ACACACTACCTGACTCCTGCAGGAGGATGAA ACAAGCCTTTCAGGGGCCGTGCAGAAG;AACTGCAACACATTGTGGGGGCCACAGGCGTT AATATCAGAAGACAGCACTCACTGCTTT";ATAGAATCCTGAGACTCCATGAAAACGCAGG Best Local Similarity 100. Matches 2191; Conservative Query Match 121 241 61 181 361 61 121 181 241 301 301 541 361 421 421 481 481 541 ò g ò g Q ò Q δ g οy q φ q ò q ò g QQ ò ò

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              AAATGAATATCTTGAATAATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAATTTAGAA 1920
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//tags a /product= "osteoprotegerin binding protein"
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97US-0880855.
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P-PSDB; W83194.
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16-APR-1997;
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The present sequence encodes human osteoprotegerin (OPG) binding profein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein to osteoclast differentiation and and and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for continuous animal models, while complementary sequences are used for thistics animal models, while complementary sequences are used for online animal models, while complementary sequences are used for online animal models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPG binding protein, particularly soluble forms of OPG binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTGGCCGAGGAAGGAAGGATCGCGGAGCAGGGCGCCCGAACTCCGGGCGCCC 120
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ic acid encoding osteoprotegrin binding protein - useful for, treating bone diseases by modulating osteoclast differentiation
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                                                                                                            Claim 1; Fig 1; 47pp;
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Best Local Similarity
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1141 A	ATGTCTATACATGTGTAAGACTACTAAGF GACATGGCCCACGGTGTATGAAACTCACAGC 1200	RESI	ULT
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1201	CCTCTCTCTTGAGCCTGTACAGGTTGTGTATATGTAAAGTCCATAGGTGATGTTAGATTC 1260	Y Y	62
1234 c	nniinniinniinniinniinniinniinniinniinn	XX	25
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                                                                                                                                                  AAATGAATATCTTGAATAATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAATTTAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4A encoding a murine osteoprotegerin ligand (OPGL).
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/product= "osteoprotegerin ligand"
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> It is not capable of inducing osteoclast differentiation in the absence of CSF-I. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL anolypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other OPGL a potent osteoclast differentiation factor when combined with CSF-1. nseq The present sequence encodes a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. O for treating, preventing and ameliorating osteoporosis or c s or conditions characterised by excessive bone resorption. (OPGL) activity on of osteoprotegerin ligand ameliorate osteoporosis -110pp; English down-requlation treat, prevent and Page Disclosure; diseases 2

BP; 641 A; 494 C; 541 G; 623 T; 0 other; Sequence 2299

5 180 240 300 345 360 405 420 465 480 540 585 9 645 105 TAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGAC 720 9 Gaps gccaggacctctgtgaaccggtcggggcgggggccgcctggccgggaagtctgctcggcgg tgaggcccagccatttgcacacctcaccatcaatgctgccagcatcccatcgggttccca GCCAGGACCTCTGTGAACCGGTCGGGGCGGGGCCGCCTGGCCGGGAGTCTGCTCGGCGG TGGGTGGCCGAGGAAGGGAGAACGATCGCGGAGCAGGGCGCCCGAACTCCGGGCGCCG tgggtggccgaaggaaggaagaacgatcgcggagcagggcgccgaactccgggcgccg CAGCGGCCCCGGCGTCCCACACGAGGGTCCGCTGCACCCCGGGCCTTCTGCACCGGCTCC GGCGCCGCCACCCGCCGCCTCCCGCTCCATGTTCCTGGCCCTCCTGGGGGCTGGGACTGGG CCAGGTGGTCTGCAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAG TTTGCAGGACTCGACTCTGGAGAGTGAAGACACACTACCTGACTCCTGCAGGAGGATGAA ACAAGCCTTTCAGGGGGCCGTGCAGAAGGAACTGCAACACATTGTGGGGCCACAGGGGCTT acaagcctttcagggggccgtgcagaaggaactgcaacacattgtggggccacagcgctt ctcaggagctccagctatgatggaaggctcatggttggatgtggcccagcgaggcaagcc TGAGGCCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCA CGCCATGCGCCGGGCCAGCCGAGACTACGGCAAGTACCTGCGCAGCTCGGAGGAGATGGG AATATCAGAAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAAACGCAGG CTCAGGAGCTCCAGCTATGATGGAAGGCTCATGGTTGGATGTGGCCCAGCGAGGCAAGCC 5; Length Indels 21; 12; DB Score 2144.8; Pred. No. 0; 0; Mismatches Query Match 97.9%; Best Local Similarity 99.4%; Matches 2174; Conservative 46 106 166 226 241 286 346 406 466 526 541 586 121 181 301 361 421 481 601 661 61 g g g q q qq qq g οy qq g g ò ٥y ò ò οý ò ò Q ò

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Agonists and antagonists of TRANEE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing T cell activation. These techniques are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially CD40L or TNF-alpha).
cokines (TRANCE). Human or murine TRANCE polypeptides or their lants, fragments, derivatives or analogues may be used as modulators immune response in a mammal comprising, antisense sequences to
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RANK ligand (RANKL). RANKL polypelytides can activate RANK and can be used to induce maturation of dend:itic cells and enhance their allo-stimulatory capacity, thereb: augmenting an immune response. The soluble RANK polypeptide composition may also be used for requiating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negitive effects of an inflammatory response that result from trigger:ing of RANK, e.g. in treating toxic shock or sepsis, graft-versus-hos: reactions, or acute inflammatory cactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhilitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK expressing cells from the negative effects of chemichterapy or the presence of high levels of TANK and TANK and also the used for detection and drug
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BP; 436 A; 355 C; 3,9 G; 460 T; 0 other; Sequence 1630

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73.7%; Score 1615.8; DB 19; 99.8%; Pred. No. 0;
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        Best Local Similarity 99.8
Matches 1628; Conservative
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This cDNA encodes a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK wolly a soluble RANK which binds to used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in Inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neophastic cells that express RANK. The products can also be used in adjunct therapy for disease characterised by neophastic cells that express RANK. The products
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RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
immune response; inflammatory response; toxic shock; sepsis;
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                            RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
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07-MAR-1997;
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 ACTCGACTCTGGAGAGTGAAGACACACTGACTGACTGCAGGAGGATGAAAGCCT
                                                     TTCAGGGGGCCGTGCAGAAGGAACTGCAACACATTGTGGGGCCCACAGCGCTTCTCAGGAG
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factor; OCIF; OCIF-binding molecule; OBM
tctor bone disorder; calcium metabolism;
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                                                                                              TAGTATTTGATTCAAAATATTTAAAAATG:;CTCACTGTTGACATATTTAATGTTTTAAAT
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I, Yano K, Yasuda H;
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absorption factors such as calcitriol or parathyroid hormone (PTH).

OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
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                                                                                                                                                                             Length 1538;
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                                                                                                                                       Sequence 1538 BP; 382 A; 381 C; 416 G; 359 T; 0 other;
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Pred. No. 0;
0; Mismatches
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99.98;
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Matches 1537; Conservative
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ttgctttcggcatcatgaaacatcgggaagcgtacctacagactatcttcagctgatggt
                        CACGAAAAACTGGTCGGCCAATTCTGAATTCCACTTTTATTCCATAAATGTTGGGGGATT
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                                                                                                                                                                                                                                                                                                                                                          tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a human osteoprotegerin ligand (OPGL).
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The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce in immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
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76.3%; Pred. No. 3.7e-253;
ive 0; Mismatches 437; Indels
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Human, osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor;
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        TCAGGTGTAATGTTTTCTGTAAAGTTTTGTAAATTATATTTGTGCTATAGTATTTGAT
                               TCAAAATATTTAAAAATGTCTCACTGTTGACATATTTAATGTTTAAATGTACAGATGTA
                                       TTTAACTGGTGCACTTTGTAATTCCCCTG-----AAGGTACTCGTAGCTAAGGGGGCAGA
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Host cells transfected with vectors containing nucleic acid molecules encoding OPC binding protein are used to produce recombinant OPC binding protein. OPC binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding open binding protein can be used to detect OPC binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of present sequence encodes human osteoprotegerin (OPG) binding protein. binding protein, particularly soluble forms of OPG binding protein Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, e loss caused by arthritis or metastases, hypercalcaemia, Paget's asse, periodontal disease, osteoporosis, lossening of prostheses, Nucleic acid encoding osteoprotegrin binding protein – useful for, e.g. treating bone diseases by modulating osteoclast differentiation optionally in combination with agents that promote bone growth. Claim 1; Fig 4; 47pp; English. 98US-0052521. 97US-0842842. 97US-0880855. WPI; 1998-594578/50 (AMGE-) AMGEN INC diagnosis P-PSDB; W83195 30-MAR-1998; 6-APR-1997; 23-JUN-1997; WJ; e.g. trea disease, Ab, Boyle bone OPG \$\times_{\time

Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

20; 153 213 273 333 390 393 450 510 Gaps 95 CAGGGCGCCCGAACTCCGGGCGCC - - GCGCCATGCGCCGGGCCAGGCCGAGACTACGGCAA CCTGGCCCTCCTGGGGCTGGGACTGGGCCAGGTGTCTGCAGCATCGCTCTGTTCCTGTA GTACCTGCGCAGCTCGGAGGAGATGGGCAGCGGCCCCCGGCGTCCCACACGAGGGTCCGCT GCACCCGCGCCTTCTGCACCGGCTCCGGCGCCGCCACCCGCCGCCTCCCGCTCCATGTT DB 19; Length 2274; 78; 437; Indels 51.1%; Score 1118.8; DB 1976.3%; Pred. No. 3.7e-253; ive 0; Mismatches 437; Best Local Similarity 76.3%; Matches 1659; Conservative Query Match 36 154 154 214 274 274 331 334 391 394 451 g 셤 οy g ŏ qq δ ρp ò δ

1107 1520 ITTTTTTTTTTTAATGAGGAGAGAAAATATATGTATTTTTATATAATGTCTAAAGTTATATT 1579 750 747 627 807 867 927 987 567 687 1228 ctactaagaggcatggccccaacggtacacgactcagtatccatgctcttgaccttgtag 1460 AGTGTGAAGGGTTAAGTTCTTTTGAATTGTTACATTGCGCTGGGACCTGCAAATAAGTTC catctgaaggggcaaattcttttgaattgttacatcatgctggaacctgcaaaaaatc-1288 agaacacgcgtatttacagccagtgggagatgttagactcatggtgtgttacacaatggt 1340 TTATGAAAAACTTACACGTGAGCTATGGAAGGGGGGTCACAGTCTCTGGGTCTAACCCCTG CGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTAAGCAAACGGAAAACTAAGGGTTAA CCCAAGTTCTCATAACCTGATGAAAGGAGGAGCACGAAAAAACTGGTCGGGCAATTCTGA 1051 cagcatcgaggtctccaacccctccttactggatccggatcaggatgcaacatactttgg 1111 ggcttttaaagttcgagatatagattgagccccagtttttggagtgtt---atgtatttc CTACTAAGAGACATGGCCCACGGTGTATGAAACTCACAGCCCTCTCTTGAGCCTGTAC AGGTTGTGTATATGTAAAGTCCATAGGTGATGTTAGATTCATGGTG-ATTACACACGGT 1280 TTTACAATTTTGTAATGATTTCCTAAGAATTGAACCAGATTGGGAGAGGTATTCCGATGC ttttaaattttgtaatgaattcct-agaattaaaccagattggagcaattacgggttgac GACATGTGCCACTGAGAACCTTGAAATTAAGAAGATGCCATGTCATTGCAAAGAAATGAT 1451 gtcatgtgccccttcgcagct-gaagtggagagggtgtcatct-agcgcaattgaaggat aaaattaatacctgattcatgtaggagaattaaacaggcctttcaaggagctgtgcaaaa CATCAATGCTGCCAGCATCCCATCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCA CCAAGATGGCTTCTATTACCTGTACGCCAACATTTGCTTTCGGCATCATGAAACATCGGG AAGCGTACCTACAGACTATCTTCAGCTGATGGTGTATGTCGTTAAAACCAGCATCAAAAT ATTCCACTTTTATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAT GGCTTTCAAAGTTCAGGACATAGACTGAGACTCATTTCGTGGAACATTAGCATGGATGTC 1108 CTAGATGTTTGGAAACTTCTTAAAAA-----ATGGATGATGTCTATACATGTGTAAAGA ----ACTACCTGACTCCTGCAGGAGGATGAAACAAGCCTTTCAGGGGGCCGTGCAGAA GGAACTGCAACACATTGTGGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGG CTCATGGTTGGATGTGGCCCAGCGAGGCAAGCCTGAGGCCCAGCCATTTGCACACCTCAC 988 TAGCATTCAGGTGTCCAACCCTTCCCTGGTGGATCCGGATCAAGATGCGACGTACTTTGG cttatgagaaactgcatgtgggctatgggagggg-__ __ __ __ 1400 748 868 928 1348 1407 1048 1221 571 628 688 808 568 1161 454 셤 g Dp Pp qq g g g g qq q g q g g ōλ òλ δ d ò QΥ 셤 à à δ ò ò ŏ δy δy ÓΥ QΥ οy δy

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                                                                                              TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytckine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
                       TCAGGTGTAATGTTTTCTGTGCAAAGTTT!GTAAATTATTTTGTGCTATAGTATTTGAT
                                                                TTTAACTGGTGCACTTTGTAATTCCCCTG· ----AAGGTACTCGTAGCTAAGGGGGCCAGA
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Pred. No. 2.8e-215;
); Mismatches 358; Indels 71;
                                                                                                                                                                                                                              cancer
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Conservative 0;
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98US-0989479.
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                                                                      GTTCAGGACATAGACTGAGACTCATTTCGTGGAACATTAGCATGGATGTCCTAGATGTTT
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                               TATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAG
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bone absorption factor; bone disorder; calcium metabolism;
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                                                                                                                         atagaaaagttattagtggtttatcagc----aaaaaagtccaattttaatttagtaaat
                                             TTGAACAGGTGTCTTTTTTTTACAAGAGCTACAAATTGTAAATTTTTGTTTCTTTTTTTCC
                                                                                            CATAGAAAATGTACTATAGTTTATCAGCCAAAAAACAATCCACTTTTTAATTTAGTGAAA
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Tsuda E;
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Tomoyasu A,
Yasuda H;
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Nakagawa N, Shima N, Takahashi K, Tomoy
Washida N, Yamaguchi K, Yano K, Yasuda
                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of the specification.
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                                                                                                            V69900 standard; cDNA to mRNA;
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97JP-0097808
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97JP-0217897
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09-JUN-1997;
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Sat

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activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay
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                                  diagnostic purposes, and as
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Osteoprotegerin is a secreted member of the tumour necrosis factor. Teceptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The mutine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-I. It is not capable of inducing osteoclast differentiation in the absence of CSF-I. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPGL activity in an animal. The method comprises using at least one OPGI polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of osteoprotegerin ligand (OPGL) activity used
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                                                                                                                                                                                                                          Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conditions characterised by excessive bone resorption.
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                                                                                                                                                                                               DNA encoding a murine osteoprotegerin ligand (OPGL).
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iive 0; Mismatches 0;
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                               caggactcgactctggagagtgaagacacactacctgactcctgcaggaggatgaaacaa
                                                                                                                                                                           AAGCTCCGAGCTGGTGAAAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCG
                                                          GTGGTCTGCAGCATCGCTCTGTTCCTGTACTTTCCAGCGCAGATGGATCCTAACAGAATA
                                                                                     TCAGAAGACAGCACTCACTGCTTTTATAGAATCCTGAGACTCCATGAAAACGCAGGTTTG
                                                                                                   tcagaagacagcactcactgcttttatagaatcctgagactccatgaaaacgcaggtttg
                                                                                                               CAGGACTCGACTCTGGAGAGTGAAGACACACTACCTGACTCCTGCAGGAGGATGAAACAA
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This sequence encodes the osteoclast formation promoting factor (OBM). The invention relates to an OBM binding protein (OBM-BP). The protein is useful as a preventive and/or treating agent for bone metabolic diseases such as osteoporosis. Substances which inhibit the binding of OBM to OBM-BP can be used as biochemical reagents.
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            AGCAACGGAAAACTAAGGGTTAACCAAG? TGGCTTCTATTACCTGTACGCCAACATTTGC
                                    TTTCGGCATCATGAAACATCGGGAAGCG1 ACCTACAGACTATCTTCAGCTGATGGTGTAT
                                                                  GTCGTTAAAACCAGCATCAAAATCCCAAK TTCTCATAACCTGATGAAAGGAGGGAGCACG
                                                                                                 AAAAACTGGTCGGGCAATTCTGAATTCCI/CTTTTATTCCATAAATGTTGGGGGGATTTTTC
                                                                                                                                AAGCTCCGAGCTGGTGAAGAAATTAGCA%TCAGGTGTCCAACCCTTCCCTGCTGGATCCG
                                                                                                                                                              GATCAAGATGCGACGTACTTTGGGGCCTTTCAAAGTTCAGGACATAGACTGA 1075
                                                                                                                                                                      pone
                                                                                                                                                                                                                                                               Nucleic acid encoding a murine OC..F-binding molecule (OBM).
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Takahashi (, Tomoyasu A,
. K, Yano K, Yasuda H;
                                                                                                                                                                                                                  V69898 standard; cDNA to mRNA; 73! BP
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97JP-0217897.
97JP-0224803.
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Nakagawa N, Shima N,
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The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol. or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological
                                                                                                                                                                    activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as components of drugs.
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Pred. No. 2.7e-163;
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100.0%; Pred. No. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting a inflammatory response and for protection of cells
                                                                                                                                                                                                                                                   RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This cDNA encodes a human RANKL, a ligand for the RANK (receptor
                                                                                                                                                                                                       NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for RANK)"
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                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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96US-0059978.
97US-0813509.
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2

Gaps

6

Indels

0; Mismatches 158;

Score 666.2; DB 19; Length 954; Pred. No. 4.2e-147;

30.48;

Query Match 30.4 Best Local Similarity 82.5 Matches 790; Conservative

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TTTTTCAAGCTCCGAGCTGGTGAAGAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTG 1018
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ATGCGCCGGGCCAGACTACGGCAAGTACCTGCGCAGCTCGGAGGAGATGGGCAGC
                                                                                                                                                                                               GTGGTCTGCAGCATCGCTGTTCCTGTACTTTCGAGCGCAGATGGATCGAACAGAATA
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                                                                                  178 gttgtctgcagcytcgccctgttcttctatttcagagcgcagatggatcctaatagaata
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                                                                                                                                                                                                                                                                                                                                 425 CAGGACTCGACTCTGGAGAGTGAAGACAC-----ACTACCTGACTCCTGCAGGAGGATG
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                                                                                                                                245 CCGCCACCCGCCCCCCCCCCCCTCCATGTTCCTGGCCCTCCTGGGGCTGGGACTGGGCCAG
                                                                                                                                               AAACAAGCCTTTCAGGGGCCGTGCAGAAGGAACTGCAACACATTGTGGGGCCACAGCGC
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61 TGGGTGGCCGAGGAAGGGAGAAGATCGCGGAGCAGGCGCCCCGAACTCCGGGCGCGC 120
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                                                                     Sequence 30,
Sequence 1,
Sequence 5,
Patent No. 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: BOYLE, William J.
TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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                                                                                                                                        US-08-553-619B-8
US-08-927-394-1
US-07-867-106-2
US-08-724-394A-20
US-08-724-394A-21
US-08-724-394A-21
US-08-486-342-1
                US-07-991-867B-1
US-08-544-332-1
US-08-924-747-25
US-08-633-993A-30
US-09-633-930-613-1
US-08-319-704-5
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US-08-066-371-1
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Pred. No. 0;
0; Mismatches
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Patent No. 5843678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.4%;
Matches 2174; Conservative 0
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1840 Dehavilland
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MEDIUM TYPE: Floppy disk
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2295 base pairs
6768
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STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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CITY: Thousand Oaks
STATE: California
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US-08-842-842-6
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                                                                                                                                                                                                                 2191
1 GCCAGGACCTCTGTGAACCG.......TTTTGGTACTTAAAAATGGC 2191
                                                                                                                           ; Search time 147.31 Seconds
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Sequence 3
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/ED_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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                                   Compugen Ltd.
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US-08-996-139-12

US-08-996-139-12

US-08-670-354-3

PCT-US96-10895-3

US-08-670-354-1

PCT-US96-10895-1

US-08-670-354-5

PCT-US96-10895-1

US-08-670-354-5

PCT-US96-10895-1

US-08-458-1

US-08-487-8268-11

US-08-487-8268-13

US-08-487-8268-13

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US-08-913-842-3
US-08-446-855A-1
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                                         December 28, 2000, 17:40:57
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                                                                                       - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Oy Dp	121	CGCCATGCGCCGGGCCAGCCGAGACTACGGCAAGTACCTGCGCAGCTCGGAGGAGATGGG 180
Oy Dp	181	CAGCGCCCCGGCGTCCCACACGAGGGT(;CGCTGCACCCGGCCTTCTGCACCGGCTCC 240
Qy Db	241	GGCGCCGCCACCCGCCCTCCCGCTCCLAGTTCCTGGCCCTCCTGGGGCTGGGACTGGG 300
Qy Db	301	CCAGGIGGTCTGCAGCATCGCTCTGTTC(!TGTACTTTCGAGCGCAGATGGATCCTAACAG 360
Oy Db	361	42
Qy Dp	421	TTTGCAGGACTCGACTCTGGAGAGTGAA(JACACACTACCTGACTCCTGCAGGAGGATGAA 480
Qy Db	481	ACAAGCCTTTCAGGGGCCGTGCAGAAGGAACTGCAACATTGTGGGGCCACAGCGCTT 540
Oy Db	541	CTCAGGAGCTCCAGCTATGATGGAAGGC:'CATGGTTGGATGTGGCCCAGCGAGGCAAGCC 600
QY	601	TGAGGCCCAGCCATTTGCACACCTCACCATCATGCTGCCAGCATCCCATCGGGTTCCCA 660
Qy	661	TAAAGTCACTCTGTCCTCTTGGTACCAC(IATCGAGGCTGGGCCAAGATCTCTAACATGAC 720°
Qy Db	721	GTTAAGCAACGGAAAACTAAGGGTTAAC(!AAGATGGCTTCTATTACCTGTACGCCAACAT 780
Qy Db	781	TTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT 840
Qy	841	GTATGTCGTTAAAACCAGCATCAAAATC(:CAAGTTCTCATAACCTGATGAAAGGAGGGG 900
Qy Db	901	CACGAAAAACTGGTCGGGCAATTCTGAA: TCCACTTTTATTCCATAAATGTTGGGGGATT 960
Qy	961	TITCAAGCICCGAGCTGGTGAAGAATINGCATICAGGTGTCCAACCCTTCCCTGCTGGA 1020
Qy Db	1021	TCCGGATCAAGATGCGACGTACTTTGGG(CTTTCAAAGTTCAGGACATAGACTGAGACTC 1080
Qy	1081	ATTICTIGGAACATTAGCATGGATGTCC:'AGATGTTTGGAAACTTCTTAAAAAATGGAFG 1140
0y	1141	ATGTCTATACATGTGTAAGACTACTAAGAGACATGCCCACGGTGTATGAAACTCACAGC 1200

1440 1472 1500 1560 1800 1860 1980 2040 1680 1712 1772 1892 2100 1592 1652 1952 2011 ATGTCTATACATGTGTAAGACTACTAGAGACATGGCCCACGGTGTATGAAACTCACAGC 1233 2191 CCTCTCTCTTGAGCCTGTACAGGTTGTGTATATGTAAAGTCCATAGGTGATGGTTAGATTC TAAATTTTGTTTCTTTTTCCCATAGAAATGTACTATAGTTTATCAGCCAAAAAACA ATCCACTTTTTAATTTAGTGAAAGTTATTTTTTTATTACTGTACAATAAAAGCATTGTTTC GTCATTGCAAAGAAATGATAGTGTGAAGGGTTAAGTTCTTTTGAATTGTTACATTGCGCT TAATGTCTAAAGTTATATTTCAGGTGTAATGTTTTCTGTGCAAAGTTTTGTAAATTATAT AAATGAATATCTTGAATAATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAATTTAGAA GCTAATTGACTTTAGGAGCTGACATAGCCAAAAAGGATACATAATAGGCTACTGAAAATC 2188 2219 TGAATGCCATTTTTTGGTACTTAAAAAT 2041 1174 1353 1413 1441 1473 1501 1533 1561 1593 1653 1713 1741 1773 1801 1833 1861 1893 1921 1953 1981 2012 2072 2101 2132 2161 1201 1234 1261 1294 1321 1381 1621 1681 g ò ò a ò q ó q ò g ò Q ò QQ ŏ g δ qq οy g οy Ω ò QQ ò g δ a ò Q g ò ò

RESULT 2 US-08-996-139-10 us-08-989-362-1.rni

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TCTAACCCCTGGACATGTGCCACTGAGAACTTAAGAAGATGCCATGTCATTGC 1448
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                                                                                                                                                                                                                                                         COMPUTER FALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILLING DATE: 22 DECEMBER 1997
CLASSIFICATION:
                                                                                                                                                    ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
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                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/772,330
FILING DATE: 23 DECEMBER 1996
ATTONEY, FAGENT INFORMATION:
NAME: PERKINS, PALTICIA ANDE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHHONE: (206)587-0644
                                                APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
Sequence 10, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 1630 base pairs TYPE: nucleic acid STRANDEDNESS: single
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IMMEDIATE SOURCE:
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Best Local Similarity 99.89

Matches 1628; Conservative
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US-08-996-139-10
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                                                                                              1380 AAAGTTATATTTCAGGTGTAATGTTTTC;GTGCAAAGTTTTGTAAATTATATTTGTGCTA
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APPLICANT: Galibert, Laurent
APPLICANT: Galibert, Laurent
APPLICANT: Marsakovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation. Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: Apple Power Macintos;
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
AND APPLICATION DATA:

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REGISTRATION NUMBER: 34,693
REPERENCE/DOCKET NUMBER: 2851-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEPRAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/08996139 Patent No. 6017729 GENERAL INFORMATION:
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TELEFAX: (
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82.5%; Pred. No. 2e-153;
tive 0; Mismatches 158;
                                                                                                                                                                                                                                                                 LIBRARY:
CLONE: huRANKL (full length)
                SEQUENCE CHARACTERISTICS:
LENGTH: 954'base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
INFORMATION FOR SEQ ID NO:
                                                                                       single
                                                               TYPE: nucleic ació
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMG
                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                              US-08-996-139-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           790;
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Best Local S
Matches 790
                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                    778 AGCACCAAGTATTGGTCAGGGAATTCTGAATTCCATTTTTTATTCCATAAACGTTGGTGGA 837
                                                                                                                                                                 GTGTACGTCACTAAAACCAGCATCAAAATCCCAAGTTCTCATACCCTGATGAAGGAGGA 777
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APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1013 CIGCTGGATCCGGATCAAGAIGCGACGIACTITGGGGGCTITCAAAGIT 1060
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Pred. No. 3.4e-05;
0; Mismatches 171; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 2
LENGTH: 1042
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08584031A Patent No. 6030945
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Patent No. 6046048
                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: ASKHORAZI, AVI J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22US03
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50.0%;
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US-08-584-031-2
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Best Local Similarity
Matches 174; Conserv
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GGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCTTCC 1012
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APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: OYLOKINE That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 58.4; DB 5; Best Local Similarity 50.0%; Pred. No. 3.4e-05; Matches 174; Conservative 0; Mismatches 171;
                                                                                                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                   SOFTWARE: Winparin (Genericch)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MATECHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0978P1
TELECOMMUNICATION INFORMATION:
                                                                Bruno Blvd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Kathryn A. Anderson,
STREET: 51 University Street
                                                                                                                                                                                                                                                                 PC-DOS/MS-DOS
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STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
ZIONTEX: 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 415/225-5416
TELERAX: 415/95-9881
TELES: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1042 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                         COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                              ZIP: 94080
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Seattle

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713 AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 772
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                                                                                                                                                                           ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
                                                                                      APPLICANT: Immunex Corporation.
TITLE OF INVENTION: CYTCKING That Induces Apoptosis CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 171;
                                                                                                                                                                                         STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ITP: 98101
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        омыек: PCT/US96/10895
25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/548,368 FILING DATE: 01-NOV-1995 CLASSIFICATION:
                                          Sequence 3, Application PC/TUS9610895 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: ANGERSON, KASHLYUN A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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LOCATION: 78..383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 174; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US96-10895-3
                    PCT-US96-10895-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                713 AACATGACGTTAAGCAACGGAAAACTAA;GGTTAACCAAGATGGCTTCTATTACCTGTAC 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    773 GCCAACATTTGCTTTCGGCATCATGAAA\ATCGGGAAGCGTACCTACAGACTATCTTCAG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               833 CTGATGGTGTATGTCGTTAAAACCAGCA'CCAAAATCCCAAGTTCTCATAACCTGATGAAA 892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      662 GGGGGAATATTTGAGCTTAAGGAAAATG, ICAGAATTTTTGTTTCTGTAACAAATGAGCAC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
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50.0%; Pred, No. 4.1e-05;
tive 0; Mlsmatches 171;
                                                     MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/496,532
FILING DATE: 29-JUN-1995
CLASSIFICATION NUMBER: US 08/548,868
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: US 08/548,868
FILING DATE: 01-NOV-1995
CLASSIFICATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
RECERNENCE/DECKET NUMBER: 2835-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,154
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 756822
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1521 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.7%
Best Local Similarity 50.0%
Matches 174; Conservative
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STRANDEDNESS: single
                    ZIP: 98101
COMPUTER READABLE FORM:
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US-08-670-354-3
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CLONE: HUAIC-dv
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USA
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Best Local Similarity
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                                  893 GGAGGGAGCACGAAAAACTGGTCGGCCAATTCTGAATTCCACTTTTATTCCATAAATGTT 952
                                                                                                                         1013 CTGCTGGATCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTT 1060
                                                                                                                                                                                ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Steven R. Wiley and APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-40N-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/496,632
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FRIGG DATE: 29-40N-1995
CLASSIFICATION A 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-B
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/548,368
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; Sequence 1, Application US/08670354
; Patent No. 5763223
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1751 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; LOCATION: 88..
US-08-670-354-1
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DB 2;

2.7%; Score 58.4;

Query Match

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                                                                                                    700 CAAATGGTCCAATATATTTACAAATACACAAGTTATCCTGACCCTATATTGTTGATGAAA 759
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                                                                        AACATGACGTTAAGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTAC 772
                                                                                                                                                                     773 GCCAACATTTGCTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAG 832
                                                                                                                                                                                                                                                                  833 CTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGTTCTCATAACCTGATGAAA 892
                                                                                                                                                                                                                                                                                                                                                                    893 GGAGGGAGCACGAAAAACTGGTCGGCCAATTCTGAATTCCACTTTTATTCCATAAATGTT 952
                           3; Gaps
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tive 0; Mismatches 171; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine That Induces Apoptosis
UNUBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
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APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION UNBER: US 08/548,368
APPLICATION UNBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION THEORMATION:
NAME: ATTORNEY/AGENT INFORMATION:
NAME: ANGERSON, Kathryn A.
REGISTRATION NUMBER: 32,172
RETERENCE/DCCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application PC/TUS9610895 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 233-0644
TELEEX: 756822
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                      Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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PCT-US96-10895-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     760 AGTGCTAGAAATAGTTGTTGGTCTAAAGFTGCAGAATATGGACTCTATTCCATCTATCAA 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       713 AACATGACGTTAAGCAACGGAAAACTAAKKGGTTAACCAAGATGGCTTCTATTACCTGTAC 772
                                                                                                                                                                                                                                                                                                                            583 AACTIGCACTIGAGGAAIGGIGAACTGGICAICCAIGAAAAAGGGITIIIACTACATCIAI 642
                                                                                                                                                                                                                                                                                                                                                                773 GCCAACATTTGGTTTTGGGCATCATGAAA(ATCGGGAAGGGTACCTACAGACTATCTTCAG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                             833 CTGATGGTGTATGTCGTTAAAACCAGCAJCAAAATCCCAAGTTCTCATAACCTGATGAAA 892
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                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                               Length 1751;
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STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08670354
Patent No. 576323
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: CYLOKINE That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             Scort 58.4; DB 6;
Pred No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DAMA:
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APPLICATION UNBER: US 08/496,632
FILING DATE: 29-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION PAR:
APPLICATION NUMBER: US 08/548,358
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/670,354 FILING DATE: 25-JUN-1996 CLASSIFICATION: 435
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50.0%;
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MOLECULE TYPE: CDNA to mRNA
                                                                                                                                                                                                                                               Matches 174; Conservative
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                                 ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: huAIC
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                     HYPOTHETICAL:
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ZIP: 98101
                                                                                                              ; NAME/KEY:
; LOCATION:
PCT-US96-10895-1
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STATE:
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951 TTGGGGGATTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCTT 1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 54; DB 2; Length 1366;
51.7%; Pred. No. 0.00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Immunex Corporation.
TITLE OF INVENTION: CYTCKINE That Induces Apoptosis
CORRESPONDENCE: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
          NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/CHOCKET WUMBER: 2835-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELERX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMBER: PCT/US96/10895
25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application PC/TUS9610895 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         LENGTH: 1366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 51.73
Matches 123; Conservative
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                                                                                                                                                                                                                                                      linear
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IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY:
, LOCATION:
US-08-670-354-5
                                                                                                                                                                                                                                                      TOPOLOGY:
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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas B.
APPLICANT: Wellems, Thomas B.
APPLICANT: ADDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1786 ITCTITATICITITAACITAATAGAGICTICAGACTIGICAAAACTATGCAAGAAT 1845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1726 CTGAAGGTACTCGTAGCTAAGGGGGCAGAATACTGTTTCTGGTGACCACATGTAGTTTAT 1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.3%; Score 51.4; DB 3; Length 8220;
49.1%; Pred. No. 0.0047;
tive 0; Mismatches 141; Indels 0
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1846 AAATAAATAAAATAAAATGAATATCTTGAATAATAA 1882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                     CORRELIATION DATA:
CORRELIATION UNBER: US/08/568,459A
FILING DATE: 07-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISraelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 101121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPAN: (619) 235-850
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARRATERISTICS:
LENGTH: 8220 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum
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Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 2.3
Best Local Similarity 49.1
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Patent No. 5849306

GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitais, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Waller, Louis H.
APPLICANT: Waller, David S.
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING PASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     831 AGCTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGTTCTCATAACCTGATGA 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    891 AAGGAGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCCACTTTTATTCCATAAATG 950
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51.7%; Pred. No. 0.00046;
tive 0; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th Floor
                                                                                                             NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELERX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO
                                                                                          ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                          LENGTH: 1366 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 51.79
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) NAME/KEY: CDS
) LOCATION: 47..919
PCT-US96-10895-5
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                             FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
ANTI-SENSE: N
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                          FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
                                                                                                                                        PC-DOS/MS-DOS
                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                             Floppy disk
                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chitnis,
APPLICANT: Miller, LA
APPLICANT: Peterson,
APPLICANT: Su, Xin-z
APPLICANT: Wellems,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
Matches 136; Conserv
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US-08-487-826B-13
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APPLICANT: Chitchs, Chetan
APPLICANT: Milor, Louis H.
APPLICANT: Milor, Louis H.
APPLICANT: Beterson, David S.
APPLICANT: Bu, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMA INS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1726 CTGAAGGTACTCGTAGCTAAGGGGGCCAG, IATACTGTTTCTGGTGACCACATGTAGTTTAT 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1786 ITCTTTATTCTTTTAACTTAATAGAGTUTTCAGACTTGTCAAAACTATGCAAGCAAAAT 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8086 ATGTATTTATATAAAAAGAAATATAA,\AACAAATTTATTAAAATGAAAAAAGAAAA 8145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1666 TIGACATATITAATGTTTTAAATGTACA;ATGTATTTAACTGGTGCACTTTGTAATTCCC 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7966 TATATGTGTTTTTGGATATATATATGTGNATGTATATGATTTTCTGTATATATGTATTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.3%; Scor: 51.4; DB 4; Length 8220; Best Local Similarity 49.1%; Pred. No. 0.0047; Matches 136; Conservative 0; Mismatches 141; Indels 0
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO;
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487.027
FILING DATE: 10-sem 15/08/487.027
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620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                               ATICKNEI/ANDENI INFORMATION

NAME: ISraelsen, Ned
REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER: NIH12..001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8220 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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CORRESPONDENCE ADDRESS:
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California
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Peterson, David S.
Su, Xin-zhaun
Wellems, Thomas E.
VENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
VENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15286 TATATGTGTTTTTGGATATATATATGTGTATATGTATTTTCTGTATATGTATTTGTG 15345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15406 ATGTATTTATATAAAAAAGAAATATAAAAACAAATTTATTAAAAATGAAAAAAGAAAA 15465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1726 CTGAAGGTACTCGTAGCTAAGGGGGCAGAATACTGTTTCTGGTGACCACATGTAGTTTAT 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 19124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.3%; Score 51.4; DB ilarity 49.1%; Pred. No. 0.007 Conservative 0; Mismatches
NAME: ISraelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TRILEPHONE: (619) 235-0577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knobbe Martens Olson & Bear
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                                                                                                                                        TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SED ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
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Pred. No. 0.16;
0; Mismatches 337; Indels 12; Gaps
                                                                                               MEDILUM.
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION NUMBER: 29,655
ATTORNEY/AGENT INFORMATION:
NAME: ISTRAILON NUMBER: 29,655
REGISTRATION NUMBER: 29,655
REFERENCE/POCKET NUMBER: 29,655
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 45.4%
Matches 290; Conservative
                                                                    COMPUTER READABLE FORM:
California
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                                                                                            MEDIUM TYPE:
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ANTI-SENSE: NUS-08-487-826B-13
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Search completed: December 28, 2000, 19:36:11 Job time: 6914 sec

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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                  7189864 seqs, 3091403243 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of result,s predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	- [35979 us84d0	827122 HS 5256	0722 BB220722	PCI-11	B24033	B22394	B236029	HS_525	B21672	T09579	006770	R23602	V31502	59h12.	f56b11	AA504211 aa59h12.s	AQ817650 HS_5265_B	AL063921 Drosophil	BB239142 BB239142	Ω				ALU63921 Drosophil						AL097152 Drosophil) L	80	312	140	389	013	6742 Dro	9689	1206 D	85149	73
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musculus cDNA clone IMAGE:3325120
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:1069284
                                                                                1947
                                                                                                                                     2007
                                                                                                                                                  TGACCACATGTAGTTTATTTCTTTATTCTTTTAACTTAATAGAGTCTTCAGACTTGTCA
                         CCAAAAAGGATACATAATAGGCTACTGAAAATCTGTCAGGAGTATTTATGCAATTATTGA
                                                                                                                                                                                                                    420 ACAGGIGICITITITACAAGAGCIACAAATIGIAAATITIGITICITITITITICCCATA
                                                                                                                                                                                                        GAAAATGTACTATAGTTTATCAGCCAAAAAACAATCCACTTTTTAATTTAG 2118
                                                                                                                                                                                                                                                             /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3325120"
/clone_lib="Soares mouse 3NbMS"
                                                                                                                                                                                                                                                                                                                            us84g09.yl Soares mouse 3NbMS Mus. 51, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: -40RP from Gibco
High quality sequence stop: 424.
Location/Qualifiers
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/dev_stage="4 weeks"
/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 514)
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.mad.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 524) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. an
                                                                                                      1623 GTGCTATAGTATTTGATTCAAAATATTTAAAAATGTCTCACTGTTGACATATTTAATGTT 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1743 TAAGGGGCAGAATACTGTTTCTGGTGACCACGTGTAGTTTATTTGTTATTGTTTTAA 1802
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                                                                                                                                                                                                                                 61 ATGTCTAAAGTTATATTTCAGGTGTAATGTTTTCTGTGCAAAGTTTTGTAAATTATATT 120
                                                                                                                                                                                                                                                                                                                                          A0827122 524 bp DNA GSS 27-AUG-1999
HS_5256_B2_C09_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=832 Col=18 Row=F, DNA sequence.
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                                                     ä
     514;
     Length
                                                     Indels
Score 499.4; DB 35
Pred. No. 1.1e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1983 TCAGGAGTATTTATGCAATTATTGAACAGGTGTCT 2017
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                                                     0; Mismatches
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22.8%;
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                  Fax: +81-298-36-9098
                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                              /note="Vector: pB/Ce3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digsted with a combination of EcoRI and EcoRI Methylase. ilze selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           979 TGAAGAAATTAGCATTCAGGTGTCCAACC TTCCCTGCTGGATCCGGATCAAGATGCGAC 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151
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                                                                                                                                                                                                                                                                                                                     DB 103; Length 524;
                                                                                                                                       /clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                          4 others
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 131; Indels
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                                                                                                                    /db_xref="taxon:9006"
/clone="Plate=832 Col=18 Row=F"
                                                                                                                                                                                                                                                                                                                   Score 263.8; DB 1
Pred. No. 6.5e-50;
                                                                                                                                                                                                                                                        151 t
                                                                                                     /organism="Homo sapiens"
                                                           524.
http://www.htsc.washington edu
                                                       High quality sequence stop 5
Location/Qualifiers
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         Plate: 832 row: F column
Seq primer: T7
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72.8%;
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                                           Class: BAC ends
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BB220722
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Best Local Similarity
Matches 381; Conserv
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ENGATORIA MERGROS, CONTOURES, CAINTER, VARIENCE, FULTIONE, MANATIONE, MATCHER, ENGANCE, TO 313)

AUTHORS

ROUND, ALSONA, ARADIA, ARADIA, S., ARIVAMA, J., ARAGAWA, T., CORNIGIO, M. ALSONA, A., ARADIA, J., ISTINIANA, J., ISTINIANA, T., ISTINIANA, T
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7;

Gaps

26;

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Losses 1 to 306)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shiqemoto,Y., Shiqemayawa,A., Shiraki,T., Soqabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
'T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                                                                              GGGTCTAACCCCTGGACATGTGCCACTGAGAACCTTGAAATTAAGAAGATGCCATGTCAT 1445
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                                                                                                                                                                             Indels
                                                                                                                                     DB 97;
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                                                                                                                                   Score 254.2; DB Pred. No. 1e-47;
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77.98;
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                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@tojong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fr
Research Genet cs (info@tesgen.com). BAC end search page:
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Other GSSs: RPCI-11-185M9.TJ
Other GSSs: RPCI-11-185M9.TJ
Ochter Strain Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
711: 301 838 0200
Fax: 301 838 0208
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0; Mismatches 23
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/db_xref="GDB:7570952"
/db_xref="taxon:9606"
/clone="RPCI-11-185M9"
/clone_lib="RPCI-11"
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URL:http://genome.rtc.riker.go.jp,
URL:http://genome.rtc.riker.go.jp,
URL:http://genome.rtc.riker.go.jp,
Carhinci.P. Nabilyanma.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki
.N., Okazaki,Y., Muramatsu, m. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
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Y. and Hayashizaki,Y. Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Automated filtration-basec high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Haya.hizaki,Y.
KIKEN Mouse ESTS (Konno,H., et al.)
Unpublished (2000)
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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/db_xref="taxon:10090"
/clone="A600081K02"
/clone="lib="RIKEN full-length enriched, 3 days neonate
                                                                                 Contact: Yoshihide Hayashi;aki
Genome Exploration Research Group, Life Science Tsukuba Center,
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Tel: +81-298-36-9013
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/dev_stage="3 days neonate"
/lab_host="DH10B"
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyoswa, H., Kojina, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takansahi, T., Yamanaka, I.
Y., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamanara, T., Yamanaka, I.
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino,
RIKEN Mouse ESTS (Konno, H., et al.)
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Eax: +81-298-36-9018
Email: genome-researcr.riken.go.jp,
URL:http://genome-researcr.riken.go.jp,
URL:http://genome-researcr.riken.go.jp,
URL:http://genome-researcr.riken.go.jp,
URL:http://genome-researcr.riken.go.jp,
Carninci,P., Nishiyama,Y., Wastover,A., Itoh,M., Nagaoka,S., Sasaki,N., N. Okazaki,Y.
Thermostabilization and thermostrivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomatu,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB223942 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530084G16 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Carninci,P. and Hayashizaki,Y.
Confact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
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Please visit our web site (http://genome.rtc.riken.go.jp)
further details.
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/db_xref="taxon:10090"
/clone="A530084G16"
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 316)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Furdads, S., Fukunishi, Y., Hara, A., Hayatsu, N.,

Izawa, M., Kadota, K., Kagawa, I., Ishikawa, J., Ishikawa, T., Itoh, M.,

Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,

Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Ono, T., Owa, C., Saito, H., Sakaal, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                    /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB236029 316 bp mRNA EST 04-JUL-2000
BB236029 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630056P18 3' similar to AF019048 Mus musculus mRNA sequence.

MRNA sequence.

BB236029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1663 CTGTTGACATATTTAATGTTTTAAATGTACAGATGTATTTAACTGGTGCACTTTGTAATT 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1723 CCCCTGAAGGTACTCGTAGCTAAGGGGGCAGAATACTGTTTCTGGTGACCACATGTAGTT 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1543 AATATATGTATTTTTATATGTCTAAAGTTATATTTCAGGTGTAATGTTTTCTGTGCA 1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1783 TATTICITTATICITITTAACITAATAGAGICTICAGACITGICAAAACIATGCAAGC 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260 TATTTCTTTATTCTTTTAACTTAATAGAGTCTTCAGACTTGTCAAAACTATGCAACC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 28; Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 243.6; DB 28; Length
Pred. No. 2.4e-45;
0; Mismatches 34; Indels
/tissue_type="aorta and vein"
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                     /dev_stage="adult"
/lab_host="DH10B"
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88.6%;
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Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            house mouse.
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BB236029
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Fmail: genome-resertc.riken.go.jp,
URL:http://genome-resertc.riken.go.jp,
URL:http://genome-rtc.riken.go.jp/
Carhinci.p., Nishiyama.y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayshizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayshizaki,Y., Abibata,Y., Ozawa,Y., Muramatsu,M., Okazaki, Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Haysshizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Gribublished (2000)

Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was GAGAGAGAGAGCACCAAGAGCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                            Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib-"RIKEN full·length enriched, 3 days neonate thymus"
                                                                                                                                                                                                     Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1894 GTCACCAGGTGCCTTTCAAATTTAGAAGCTAATTGACTTTAGGAGCTGACATAGCCAAAA 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1954 AGGATACATAATAGGCTACTGAAAATCTGTCAGGAGTATTTATGCAATTATTGAACAGGT
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                                                                                                                                                                                                                                                                                                           3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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89.8%; Pred. No. 9.6e-44;
Micmatches 29;
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/lab_host="DH10B"
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/clone="A630056P18"
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                                                                                                              TITLE
JOURNAL
COMMENT
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1104 TGTCCTAGATGTTTGGAAACTTCTTAAAAA-----ATGGATGATGTCTATACATGTGT 1156
                                                                                                                                                                                                                                                                                                                                               1157 AAGACTACTAAGAGACATGGCCCACGGTGTATGAAACTCACAGCCCTCTCTTTGAGCCT 1216
                                                                                                                                                                                                                                                                                                                                                                                                                         1217 GTACAGGTTGTGTATATGTAAAGTCCATAGGTGATGTTAGATTCATGGTG-ATTACACAA 1275
AAATCGCAAGTTCTCATACCNTGATGAAAGGAGCAAGCACCAAGTATTGGTCAGGGAATT 408
                                                                                                                                                                                                                                                                                                                                                                   CTGAATTCCACTTTTATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAGCTGGTGAAG
                                                                                                                                                                                           1044 TTGGGGCTTTCAAAGTTCAGGACATAGACTGAGACTCATTTCGTGGAACATTAGCATGGA
                                                                                                                                                                                                                                                                                          984 AAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCGGATCAAGATGCGACGTACT
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VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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467
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AUTHORS
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holzman, T., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center University of Washington University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3818 Fax: (206) 616-3887 Email: jwallacedu, washington.edu Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library availability, please contact Pieter de Jong (pieterédejong.med.buffalo.edu, Clones may be purchased from BACPAC Resources (http://bocpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (infoéresgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                      GTACTATAGTTTATCAGCCAAAAAACAA;CCACTTTTTAATTTAGTGAAAGTTATTTAT 2133
                                                                                                                                  242
                                                                                                                                                                                                                                                                                                  AQ827168 529 bp DNIA GSS 27-AUG-1999 HS_5256_B2_G09_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=832 CO.=18 Row=N, DNA sequence.
                               Gaps
             GTCTTTTTTTACAAGAGCTACAAATTGT.\AATTTTGTTTCTTTTTTTTTCCCATAGAAAT
                                                                                                          2134 TATACTGTACAATAAAAGCATTGTTTCTGAATGGCATTTTTTGGTACTTAAAAAT 2188
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                                                                                                                                                                                     scanning the human genome
Proc. Natl. Acad. Sci. U. t. A. 96 (17), 9739-9744 (1999) 99380589
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Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=832 Col=18 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.7e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.htsc.washington.edu
Plate: 832 row: N column: 18
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chorda!a;
Mammalia; Eutheria; Primatus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: :
Location/Qualifiers
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AQ827168.1 GI:5793230
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 288)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fekuda, S., Fukunishi, Y., Hara, A., Hayara, N., Hara, C., Kadwa, T., Ishikawa, J., Ishikawa, J., Ishikawa, T., Carninci, M., Kajima, Y., Kadawa, I., Kaji, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, R., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, Y., Shigemoto, Y., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Rikin Mouse Ests (Konno, H., et al.)
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URL:http://genome.rtc.riken.go.jp,
Carninci.P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
'N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
BB216722 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530038L03 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
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Fax: +81-298-36-9098
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Contact: Yoshihide Hayashizaki
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864 AAATCCCAAGTTCTCATAACCTGATGAAA 3GAGGGAGCACGAAAAACTGGTCGGGCAATT 923

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trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                      /clone="A530038L03"
/clone_lib="RIKEN full-length enriched, adult male aorta
                                                                                                           Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                             High-efficiency full-length cDNA cloning. Methods Enzymol. 303
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/dev_stage="adult"
/lab_host="DH10B"
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BB236016 314 bp mRNA EST 05-JUL-2000 BB236016 RIKEN full-length enriched, 3 days neonate thymus Mus

DEFINITION

RESULT 11

BB236016 LOCUS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maus Musculus

Rammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1. (bases 1 to 314)

S. Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
, P., Endo, T., Hori, F., Ishi, Y., Hara, A., Hayatsu, N.,

Izawa, M., Radota, K., Ragawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Izawa, M., Radota, K., Ragawa, I., Kai, C., Kawai, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kodok, S., Kari, J., Kikuchi, N.,

Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Ono, T., Owa, C., Saitoo, H., Sakai, C., Sato, K., Shibata, Y.,

Suzuki, H., Suzuki, H., Tagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,

Suzuki, H., Suzuki, H., Tagawa, A., Shiraki, T., Yominaga, N., Toya
, T., Tsunoda, Y., Watahiki, A., Watahashi, F., Tominaga, N., Toya
, Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
,M., Muramatsu, M. and Hayashizaki, Y.

RIKEN Mouse ESTS (Konno, H., et al.)

Unpublished (2000)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J-11 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: #81-298-36-9013
Fax: #81-298-36-9018
Fax: #81-298-36-9018
Email: genome-reseatc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Thermostabilization and thermostcivation of thermolabile enzymes by trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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musculus cDNA clone A630056006 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
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/lab_host="DH10B"
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URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Vestover,A., Itoh,M., Nagaoka,S., Sasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB229867 282 bp mRNA EST 03-JUL-2000
BB229867 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus cDNA clone A630024A04 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKI,) mRNA,
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Tel: +81-298-36-9013
                                                                                                                                                                                                                                                                                32;
                                                                                                                                                                                                                          Scor: 219.8; DB 2
Pred No. 6.5e-40;
                                                                                                                                                                                                                                                                                0; M.smatches
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88.5%;
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                                                                                                           64 c
                                                                                                                                                                                                                                                                             261; Conservative
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Matches 261
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Thermostabilization and thermoactivation of thermolabile enzymes by Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh.M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
System. Genome Res. 9 (5), 463-470 (1999)
Land Hayashizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="RIKEN full-length enriched, 3 days neonate
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Pred. No. 4.8e-38;
0; Mismatches 24
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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us-08-989-362-1.rst

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 277)

2 Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozame, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N.,
Kiyoswa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kuskabe, M.,
Matsuyama, T., Miki, F., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata
Y., Shigemoto, Y., Shinagawa, A., Takamana, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.
K., Musmatsu, M., and Hayashizaki, Y., Shida, K., Yoshino,
M., Muramatsu, M., and Hayashizaki, Y.
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: Follows 1: genome-reserte.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp,
Carninci.P., Nishiyama.Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki.Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shihata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
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BB234550 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630049P08 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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/db_xref="taxon:10090"
/clone="A630049p08"
/clone_lib="RIKEN full-length enriched, 3 days neonate thynus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/dev_stage="3 days neonate"
/lab_host="DH10B"
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BB234550
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COMMENT

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Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinas; Musalia; Eutheria; Rodentia; Sciurognath; Muridae; Musinas; 1 to 316)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kani, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Kurihara, C., Kurihara, C., Shikata, Y., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Saito, H., Sato, K., Shibata, Y., Shinayawa, A., Shiraki, T., Soqabe, Y., Suqahara, Y., Suzuki, H., Taqawa, A., Takahashi, F., Tominaga, N., Toya, Y., Suzuki, H., Wataniki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Upublished (2000)

Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
1;
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BB236026 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus CDNA clone A630056P12 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor Kappa B ligand (RANKL) mRNA,
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                                                                                                                                                                                                                                                                                                                    1930 CTTTAGGAGCTGACATAGCCAAAAAGGATACATAATAGGCTACTGAAAATCTGTCAGGAG 1989
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                        Score 200.6; DB 2
Pred. No. 1.5e-35;
                                                                                                                            102 t
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URL:http://genome.rtc.riken.go.jp/
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BB236026
BB236026.1 GI:8915651
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kisunai, T., Aki/Ama, J., Shibata, K., Izawa, M., Rawai, J., Y. and Hayashizaki, Y. Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki Automated filtration-basel high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizati, Y.
High-efficiency full-leng:h CDNA cloning. Methods Enzymol. 303,
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/dev_stage="3 day: neonate"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="A630056p1;"
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2142 ACAATAAAAGCATTGTTTCTGAATGGCAT1TTTTGGTACTTAAAAAT 2188

ò a ò qq ò g Óγ q á

252 ACAATAAAAACCATTCTCTCTGAATGTTAA1TTTTTGGTACAAAAAT 298

RESULT 1 AV315022

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AV315022 251 bp mRNA EST 08-NOV-1999
AV315022 RIKEN full-length enriched, adult male thymus Mus musculus cDNA clone 5830427E05 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA
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transcriptuse and subsequently enriched for full-length by
cap-trapper. CDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 100.0. Second
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/sex="male"
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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The Institute of Physical and Chemical Research (RIKEN), Genomic
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
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/clone="5830427E05"
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Matches 197; Conservative 0; Mismatches 16; Indels 0;

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Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; . Paget's disease.
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WPI; 1998-594578/50.
N-PSDB; V70284.
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                                                                                                                                                                                                    1 MRRASRDYGKYLRSSEEMGS......LLDPDQDATYFGAFKVQDID 316
                                                                                                       December 28, 2000, 18:03:46; Search time 61.2 Seconds
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                              Compugen Ltd
                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
              GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                268485 seqs, 34193795 residues
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W59654
Y17874
Y84418
Y84419
W69956
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W68295
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Morinaga' Tsuda E;

Kobayashi F, Tomoyasu A, Yasuda H;

Kinosaki M, Takahashi K, K, Yano K,

97JP-0332241 97JP-0097808 97JP-0151434 97JP-0217897

97JP-0224803

98WO-JP01728

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The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parabyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein.
                                                                                                                                                                                                                                                                                                                                       Protein binding to osteoclastogenesis inhibitory factor - usefutor, e.g. treatment and investigation of disorders of bone and calcium metabolism
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Pages 106-108; 151pp; Japanese.
                                                                                                                                                                                       (SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                     Goto M, Higashio K,
Nakagawa N, Shima N,
Washida N, Yamaguchi
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                                                                                                                                   12-AUG-1997;
21-AUG-1997;
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                    22-OCT-1998
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                                                                                                        encoding OPG binding protein are used to produce recombinant OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrim (OG) in biological samples; to screen for specific binding agents (particularly agon.sts and antagonists, including intracellular proteins); to raises Ab (useful in immunoassays for intracellular proteins); to raises Ab (useful in immunoassays for medulate binding of OPG binding protein to osteoclast differentiation and activation receptor (ODAR). The nucleic acid molecule encoding opgoinding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for relited sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein particularly soluble forms of OPG binding protein of OPG binding protein contact or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or inetastases, hypercalcaemia, Paget's contact or acid of proteins of OPG binding protein and disease, ost.oporosis, loosening of prostheses, very
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                                                                            present sequence is human ostwoprotegerin (OPG) binding protein. cells transfected with vectoms containing nucleic acid molecules
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis
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100.0%; Pred. No. 6.4e-144;
ive 0; M.smatches 0;
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                                                Claim 19; Fig 1; 47pp; English.
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Matches 316; Conservative
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                                                                                    1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapapasrsmflallglglgg 60
                                                          1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAASRSMFLALLGLGLGQ
                                                                                                                                                                                                                                                    VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
   Length 316;
100.0%; Score 1675; DB 19; 100.0%; Pred. No. 6.4e-144;
                              0; Mismatches
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                             316; Conservative
 Query Match
Best Local Similarity
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Osteoclastogenesis inhibitory fac:or; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption facto.; bone disorder; calcium metabolism.

Unidentified WO9846644-A1

Jacob Contract

Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).

(first entry)

10-FEB-1999

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316 AA;

Sat Dec 30 09:27:16 2000

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This is the amino acid sequence of the mouse 499E9 protein, used in the method of the invention to treat conditions associated with abnormal physiclogy or development. The 499E9 protein is expressed thighly on polarised ThI T cells, binding of 499E9 to its receptor may result in either immune cell expension or apoptosis. Attagonists of 499E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatolis systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as a cute inflammatory responses in which T-cell expansion, activation or immunological r-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful in detecting or diagnosing various immunological conditions related to the expression of antigens of 499E9. The antibodies, and fragments of 499E9 can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation (e.g. cancerous conditions) or degenerative conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse cell surface antigen, 499E9 protein - used to treat conditions associated with abnormal physiology or development
                                                                                                                                                                    Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis; antagonist; autofimmune disorder; rheumatoid arthritis; systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis; acute inflammatory response; antibody; antigen; cancer.
                                                                                                                                                                                                                                                                                                                              /note= "intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                    /note= "extracellular domain"
                                                                                                                                      Amino acid sequence of mouse 499E9 protein.
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Pages 8-11; 59pp; English
                                W59654 standard; Protein; 316 AA
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                                                                                                       (first entry)
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N-PSDB; V41489.
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 Length 316;
                              Indels
   DB 19;
100.0%; Score 1675; DB 19;
100.0%; Pred. No. 6.4e-144;
ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.(
Matches 316; Conservative
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VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120 61

1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAASRSMFLALLGLGLGG 60

> a ò

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316 AA;

Sequence

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The present sequence represents murine TNF-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fargaments, derivatives or analogues may be used as modulators of immune response in a mamma comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing the life span of mature dendritic as are especially useful for treating immune system related conditions such as HIV, cancer, autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially
                                              TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen.
vvcsialflyfraqmdpnrisedsthcfyrilrlhenaglqdstlesedtlpdscrrmkg 120
                                 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK
                                                                                                                                                        VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP
                                                                                                           VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
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97US-0989479.
98US-0034099.
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                                                                                                                                                    VVCSIALFLYFRAQMDPNRISEDSTHCF; RILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
                                                                      AFQGAVQKELQHIVGPQRFSGAPAMMEG: WLDVAQRGKPEAQPFAHLTINAASIPSGSHK 180
                    Gaps
                                                9
                                                                                                                                                                                                                                                                                             Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
                                  1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGQ
                                         VTLSSWYHDRGWAKISNWTLSNGKLRVN()DGFYYLYANICFRHHETSGSVPTDYLQLMVY
                                                                                                                                tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption.
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      Length 316;
                                                                                                                                                                                                                                                                               Amino acid sequence of a murine ofteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                          /note= "tumour necrosis factor-like domain"
158..317
/note= "active ligand moiety"
                   Indels
                                                                                                                                                                                                                                                                                                                                                                             stalk domain"
   Ouery Match
100.0%; Sco.e 1675; DB 20;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 316; Conservative 0; M.Smatches 0;
                                                                                                                                                                                                                                                                                                                                                      48..71
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                            "extracellular
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                  DQDATYFGAFKVQDID 316
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02-OCT-1998;
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Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of maure osteoclasts. The specification describes a method for the in vivo down regulation of OPGL activity in an animal. The method comprises using at least one OPGL onlypeptide or subsequence, and/or at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide are lumner response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
   osteoprotegerin ligand (OPGL) activity used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAASRSMFLALLGLGLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
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                                                                                                                                                      The present sequence represents a murine osteoprotegerin ligand
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vivo down-regulation of osteoprotegerin lic
treat, prevent and ameliorate osteoporosis
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                                                                                         Claim 17; Page 81-82; 110pp; English.
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/note= "
70..157
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It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as 1 type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vivo down-regulation of osteoprotegerin ligand (OPGL) activity used treat, prevent and ameliorate osteoporosis \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 21; Length 316;
/note= "extracellular stalk domain"
                                                             /note= "active ligand moiety"
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100.0%;
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N-PSDB; 299966.
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                                                                                                                61 VVCSTALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
                                  Gaps
                                                                                     1 mrrasrdygkylrsseemgsgpgvphegplhpapsapapapapaasrsmflallglglgg 60
                                                                                                                                                                                                                                              121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK
                                                           1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPPAPAPASRSMFLALLGLGLGQ
                                                                                                                                                                                                                               VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
                                                                                                                                                                                                                                                                                     VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP
                              0;
                                 Indels
Score 1675; DB 21;
Pred. No. 6.4e-144;
; Mismatches 0;
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Best Local Similarity 100.
Matches 316; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activator of necrosis factor-rappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This represents a murine RANKL, a ligand for the RANK (receptor
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                                                                                                 NF-kB receptor activator RANK ligand (RANKL).
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Maraskovsky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Pages 55-57; 80pp; English.
W69956 standard; Protein; 294 AA.
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99.7%;
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97US-0813509.
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                                                                (first entry)
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Best Local Similarity 99.7
Matches 293; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Anderson DM,
                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                WO9828426-A2
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Pred. No. 5.3e-133;

99.78;

Best Local Similarity

Matches

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This represents a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor-kapp.B (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produke recombinant RANK protein. The soluble RANK may be used for inhibiting activation of MF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble HANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that iesult from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neophastic cells that express RANK. The products can also be used for detection and drug screening.
                   262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated receptor activator of necrosis factor-kappa B - useful for, e.g. developing products for regulating an immune or inflammatory response, treating taxic shock or sepsis
 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN
                                                                    GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                                                                                                                                                                                                 RANK; necrosis factor-kappa B; NF.kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necros:s factor; TNF; mouse.
                                                                                                                                      263 WSGNSEFHFYSINVGGFFKLRAGEEISI, VSNPSLLDPDQDATYFGAFKVQDID 316
                                                                                                                                                        NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maraskovsky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Pages 55-57; 80pp; Engilsh.
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                                                                                                                                                                                                                                                              W68292 standard; Protein; 294
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97US-0813509
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                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-377655/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; V41371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9828424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1997;
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 143
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W68292
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92.8%; Score 1554; DB 19; Length 294;

Query Match

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The present sequence is human osteoprotegerin (OPG) binding protein. Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
                                                                                                   83 DSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGA 142
                                                                                                                                                                                                          262
    Gaps
                                           Nucleic acid encoding osteoprotegrin binding protein – useful for, e.g. treating bone diseases by modulating osteoclast differentiation
                                                                                                                                                                                                       GKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMYYVVKTSIKIPSSHNLMKGGSTKN
                                                                                                                                                                                                                       23 GVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGQVVCSIALFLYFRAQMDPNRISE
                                                                                                                                             143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN
                                                                                                                                                                                                                                                                263 WSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                                                                                            Indels
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                               W83195 standard; Protein; 317
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97US-0842842.
97US-0880855.
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paget's disease.
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and activation receptor (ODAR). The nucleic acid molecule encoding OPC binding protein can be used to detect OPC binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for antisense regulation of OPC binding protein. Modulators of OPC binding protein, particularly soluble forms of OPC binding protein, particularly soluble forms of OPC binding protein or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastrases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                  VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                          HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF.
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                                                                                                                                                                                                   DB 19; Length 317;
                                                                                                                                                                                                                              31; Indels
                                                                                                                                                                                                  84.5%; Score 1417.5; DB 1984.3%; Pred. No. 1.3e-120;
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96US-0059978.
97US-0813509.
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                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                         317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                              268;
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W69957
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Care Annual and Care 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGQ
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                                                                             B - used to
inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                          isolated ligand for receptor activator of NF-kappa
                                                                                                        develop products for augmenting an immune response for inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF-kB receptor activator RANK ligand (RANKL).
                                                                                                                                                                                27; Pages 59-60; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 DPDQDATYFGAFKVQDID 316
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1998-377657/32.
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WPI; 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This represents a human RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappiB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting attivation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVCSIALFLYFRAQMDPNRISEDSTHCF'(RILRLHENAGLQDSTLESEDT - - LPDSCRRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VYVVKTSIKIPSSHNLMKGGSTKNWSGN; EFHFYSINVGGFFKLRAGEEISIQVSNPSLL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRRASRDYGKYLRSSEEMGSGPGVPHEG?LHPAPSAPAPAPAPAASRSMFLALLGLGLGG 60
                                                                                                                                                                                                                                                                                                                                                                         New isolated receptor activator of necrosis factor-kappa B - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKVTLSSWYHDRGWAKISNMTLSNGKLR'/NQDGFYYLYANICFRHHETSGSVPTDYLQLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.6%; Score 1417,5; DB 19; Length 317; 84.3%; Pred, No. 1.3e-120;
immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF.
                                                                                                                                                                                                                                                                                                                                                                                            for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
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                                                                                                                                                                                                                                                                                          Maras covsky E;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Pages 59-60; 80pp; English.
                                                                                                                                                                                   97US-0064671.
96US-0059978.
97US-0813509.
                                                                                                                                                     97WO-US23866
                                                                                                                                                                                                                                                                                       Galibert LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                        1998-377655/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AA;
                                                                                                                                                                                                                                                                                                                                        N-PSDB; V41372
                                                                                                                                                                                                                                                                                        Anderson DM,
                                                                                  WO9828424-A2
                                                  Homo sapiens
                                                                                                                                                   22-DEC-1997;
                                                                                                                                                                                      14-0CT-1997;
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                                                                                                                                                                                                        23-DEC-1996;
                                                                                                                   02-JUL-1998
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is a potent osteoclast differentiation factor when combined with CSF-1.
It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL an immune response in the animal. The method and OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vivo down-regulation of osteoprotegerin ligand (OPGL) activity used treat, prevent and ameliorate osteoporosis -  \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPAASRSMFLALLGLGLGGG 60
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                                                                                                                                                                       Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
                                                                                                                                                                                     tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 317;
                                                                                                                                     Amino acid sequence of a human osteoprotegerin ligand (OPGL).
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                                                                                                                                                                                                                                                                                                                                                             /note= "extracellular stalk domain"
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84.3%; Pred. No. 1.3e-120;
                                                                                                                                                                                                                                                                                                                           "transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                               /note= "active ligand moiety"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 78-79; 110pp; English.
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                Y84417 standard; Protein; 317
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/note=
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                                                                                                   25-JUL-2000
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                                                                  Y84417;
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RESULT 12
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12-AUG-1997;
21-AUG-1997;
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                                                                                                                                                                                                                                                                                                                 Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                 238
                                                                  239
                                                        KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
                                                                                                                                                                                                                                                                                               Osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM).
                            HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM
                 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT -- LPDSCRRM
mrrasrdytkylrgseemgggpgaphegplh-appppaaphgppaasrsmfvallglglgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein binding to osteoclastogenesis inhibitory factor - useful
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Tsuda E;
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Nakagawa N, Shima N, Takahashi K, Tomoyasu
Washida N, Yamaquchi K, Yano K, Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 36; Pages 113-114; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRAND MILK PROD CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K, Yano K,
                                                                                                                                                                                                                                          AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  97JP-0332241
97JP-0097808
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                                                                                                                                                                        DPDQDATYFGAFKVQDID 316
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form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL
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                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                     84.1%; Score 1409.5; DB 19; Length 317; 84.0%; Pred. No. 7.1e-120; ive 16; Mismatches 32; Indels 3;
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Tsuda E;
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Tomoyasu A,
Yasuda H;
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Takahashi K,
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Nakagawa N, Shima N, Takahashi K,
Washida N, Yamaguchi K, Yano K,
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97JP-0217897
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Best Local Similarity 84.0 Matches 267; Conservative
                                                                                                                                                     components of drugs
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98WO-JP01728

15-APR-1998;

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                                                                                                                 The present sequence represents an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the absorption and maturation of osteoclasts in the presence of bone absorption factors such as calcitiol or parathyroid hormone (PTH). OBM is isolated from stromm cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM; which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological exitivity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein, for investigative and diagnostic purposes, and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AQMDPNRISEDSTHCFYRILRLHENAGL(DSTLESEDTLPDSCRRMKQAFQGAVQKELQH 132
                                                                                                                                                                                                                                                                                                                                                                                                                                         133 IVGPORFSGAPAMMEGSWLDVAQRGKPE/QPFAHLTINAASIPSGSHKVTLSSWYHDRGW 192
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                                                                                                                                                                                                                                                                                                                                                                                                        193 AKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 NLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV
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                                             Protein binding to osteoclastogen.sis inhibitory factor - usef
for, e.g. treatment and investigation of disorders of bone and
                                                                                                                                                                                                                                                                                                                                             Length 244;
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                                                                                                                                                                                                                                                                                                                                            Score 1297; DB 19;
Prec. No. 7.7e-110;
0; Mismatches 0;
                                                                                             Example 28; Pages 117-119; 151pp; Japanese.
                                                                                                                                                                                                                                                                                                                                  77.4%; Scc.
100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 244; Conservative
                                                                                                                                                                                                                                                                               components of drugs.
          WPI; 1998-594563/50
                                                           for, e.g. treatment calcium metabolism
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                      N-PSDB; V69898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRMKQAFQGAVQKEL 130
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                                                                                                                                                                                                                                                                                                                                                                                                       Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and calcium metabolism
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Tsuda E;
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; Pred. No. 1.2e-92;
13; Mismatches 23;
                                                                                                                                                                                                                 Goto M, Higashio K, Kinosaki M, Kobayashi F,
Nakagawa N, Shima N, Takahashi K, Tomoyasu A,
Washida N, Yamaguchi K, Yano K, Yasuda H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 28; Pages 119-120; 151pp; Japanese
                                                                                                                                                                (SNOW ) SNOW BRAND MILK PROD CO LTD.
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84.6%;
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                           97JP-0097808
97JP-0151434
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Matches 208; Conservative
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241 kvrdid 246
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02-DEC-1997;
15-APR-1997;
09-JUN-1997;
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                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: BOYle, William J.

TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC_DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1675; DB 2;
100.0%; Pred. No. 2.2e-157;
iive 0; Mismatches 0;
US-08-477-733B-16
US-09-081-913A-16
US-08-249-189-21
US-08-844-624A-21
US-08-913A-21
US-08-913A-21
US-08-913A-21
US-08-913A-21
US-08-913A-21
US-08-41-055-2
US-08-441-055-2
US-08-441-055-2
US-08-431-055-2
US-08-477-733B-2
US-09-088-913A-2
                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/842,842 FILING DATE:
                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A-451
                                                                                                                                                                                                                                                         Sequence 7, Application US/08842842 Patent No. 5843678
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 316 amino acids
amino acid
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                                                                                                                                        1 MRRASRDYGKYLRSSEEMGS........LLDPDQDATYFGAFKVQDID 316
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                     Compugen Ltd
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US-08-763-995-2
US-09-088-913A-12
US-08-589-771B-8
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US-08-690-096-2
US-08-249-189-12
US-08-484-624A-12
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US - 07 - 940 - 605A - 2
US - 08 - 184 - 422 - 8
US - 08 - 360 - 923A - 2
US - 08 - 446 - 922 - 4
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US-08-670-354-2
US-08-584-031-1
US-08-780-496-1
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US-08-484-624A-16
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US-08-810-453-2
US-08-815-190A-2
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US-08-670-354-6
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PCT-US95-00362-5
          GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                         December 28, 2000, 18:48:36
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Maximum Match 100%
Listing first 45 summaries
                                                     sw model
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Gapop 10.0 , Gapext 0.5
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                                                    protein search, using
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length: 2000000000
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Result No. 244 173.5 173.5 173.5 173.5 171.5 17

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Minimum Maximum Database

Title: Perfect score:

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Run on:

Scoring table:

Searched:

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                                                                          143 PAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSN 202
                                                                                                                                                                                                                             COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,139
FILING DATE: 22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
WIMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Immunex Corporation, Law Department STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
84.6%; Score 1417,5; DB 3
Best Local Similarity 84.3%; Pred. No. 5.5e-132;
Matches 268; Conservative 16; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: USSN 08/772,330 FILING DATE: 23 DECEMBER 1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 60/064,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/813,509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: USSN 08/813,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Perkins, Patricia Anne
REGIGYRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2851-A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                241 VVKTSIKIPSSHNLMKGGSTKNWSGNSE) HFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTLSSWYHDRGWAKISNMTLSNGKLRVN;DGFYYLYANICFRHHETSGSVPTDYLQLMVY
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Anderson, Dirk M.
APPLICANT: Galibert, Laurent
APPLICANT: Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Act.vator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Law Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 60/06.,671
FILING DATE: 14 OCTOBER 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/81:,509
FILING DATE: 07 MARCH 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: USSN 08/77:1,330
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22 DECEMBER 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Immunex Corporation, STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08996139
Patent No. 6017729
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perkins, Patricia Anne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 28:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEÓ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 294 amino acids
                                                                                                                                                                     DQDATYFGAFKVQDID 316
                                                                                                                                                                                       301 DQDATYFGAFKVQDID 316
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                                                                                                                                                                                                                                                                                                          VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
                                                                                                                                            KOAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGS 178
                                                                                                                                                                                                                             HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLM 238
E: Kathryn A. Anderson, Immunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08670354
Patent No. 5763223
GENERAL INFORMATION:
APPLICANT: Steven R. Wiley and
APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: CYLOKine That Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM LINE APPLE MACINTOSH
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
OPERATING SYSTEM: Apple 7.5.2
OURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, KAITYN A.
REGISTRATION NUMBER: 283.172
REFERENCE/DOCKET NUMBER: 2835-B
TELECROMOUNICATION NUMBER: 2835-B
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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COMPUTER: Apple Macintosh
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MOLECULE TYPE: protein
US-08-670-354-2
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CITY: Seattle
STATE: WA
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                                                                                                        43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
                                                                                                                                                                                                              101 QDSTLESEDTLPDSCRRMKQAFQGAVQK------ELQHIVGPQRFSGAPAMM 146
                                                                                                                                                                                                                                                                                                                       EGSWLDVAQRGKPEAQPFAHLT ----INAASIPSGSHKVTL ----SSWYHDR-GWAKIS 196
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                                                                                                                                                    10 PSLGQTCVLIVIFTVLLQSLCVAVTYVXFTNELKQMQDKYSKSGIACF-----LKEDDSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 PSLGQTCVLIVIFTVLLQSLCVAVTYVFTNELKQMQDKYSKSGIACF----LKEDDSY
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     Length 281;
                                                         Indels
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15.4%; Score 258.5; DB 1; 26.4%; Pred. No. 9.8e-18; iive 54; Mismatches 113;
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APPLICANT: ASHKenazi, Avi J.
TITLE OF INVENTION: AAPO-2 LIGAND; FILE REFERENCE: 11669.220203
CURRENT APPLICATION NUMBER: US/08/584,031A
CURRENT FILING DATE: 1996-01-09; NUMBER OF SEQ ID NOS: 17
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 1, Application US/08584031A; Patent No. 6030945
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                      Best Local Similarity 26.48 Matches 78; Conservative
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Best Local Similarity 26.45
Matches 78; Conservative
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ORGANISM: Homo sapiens
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US-08-584-031-1
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US-08-780-496-1
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    STATE: W
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                                  APPLICANT: Avi Ashkenazi, Anan Cuntharapai, Kyung Jin Kim
TITLE OF INVENTION: Apo-2 Ligand
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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TITLE OF INVENTION: CYTCKINE That Induces Apoptosis NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.4%; Scort 258.5; DB 3; 26.4%; Pred No. 9.8e-18; tive 54; M.Smatches 113;
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO;
                                                                                                                                                                                                                                                                                                 SUPERALING SILLER.
SUFFRANTE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
FILING DATE: 08-Jan-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: MAISCHARG, Diane L.
REGISTRATION NUMBER: 35,600091
                                                                                                              ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Bl/d
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application PC/TUS961089999 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PO
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEGUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 26.4 Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino Acid
Patent No. 6046048
GENERAL INFORMATION:
                                                                                                                                                                                                             ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY:
US-08-780-496-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 PAASRSMFLALLGLGLGQVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kathryn A. Anderson, Immunex Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Steven R. Wiley and APPLICANT: Steven R. Wiley and APPLICANT: Raymond G. Goodwin.
TITLE OF INVENTION: Cytokine That Induces Apoptosis CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%; Score 258.5; DB 4 26.4%; Pred. No. 9.8e-18; tive 54; Mismatches 113
                                                                                                Word, Version 6.0.1
COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
                                                                                                                                                        FILING DALL.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
APPLICATION NUMBER: US 08/496,632
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Anderson, Kathryn A. REGISTRATION NUMBER: 32,172 REFERENCE/DOCKET NUMBER: 2835-WO TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-670-354-6; Sequence 6, Application US/08670354; Patent No. 5763223; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206) 587-0430
(206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 281 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein
PCT-US96-10895-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity
Matches 78; Conserva
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93 RLHENAGLQDSTLESEDTLPDSC----RRMKQAFQGAVQKELQHIVG--PQRFSGAPAMM 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ---TDEDFWDST--DGEILNRPCLQVKRQLYQLIEEVTLRTFQDTISTVPEKQLSTPPLP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL---SSWYHDR-GWAKIS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 SHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 ALKDLSFSQHFRMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 ALLGLGLGQ-----VVCSIAL------FLYFRAQMD--PNRISEDSTHCFYRIL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 NMTLSNGKLRVNQDGFYYLYANICFRHHE---TSGSVPTDYL---QLMVYVVKTSIKIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 291;
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Pred. No. 2.8e-16;
0; Mismatches 111; Indels
                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
      Cytokine That Induces Apoptosis
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                            US 08/496,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFRENCE/DOCKET NUMBER: 2835
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.6%; Sco
27.5%; Pre
tive 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 29-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 291 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.59
Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein PCT-US96-10895-6
      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                           Seattle
                                                                                                                                                       USA
                                                                                                                                                                      98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                         CITY: Sea
STATE: Wi
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 ---TDEDFWDST--DGEILNRPCLQVKRQLYQLIEEVTLRTFQDTISTVPEKQLSTPPLP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 EGSWLDVAQRGKPEAQPFAHLT ----INAASIPSGSHKVTL ----SSWYHDR-GWAKIS 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NMTLSNGKLRVNQDGFYYLYANICFRHHE---TSGSVPTDYL---QLMYYVVKTSIKIPS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 SHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.6%; Score 244; DB 1; Length 291;
Best Local Similarity 27.5%; Pred. No. 2.8e-16;
Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ALLGLGLGQ-----VVCSIAL------FLYFRAQMD--PNRISEDSTHCFYRIL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 ALKDLSFSQHFRMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK-- 63
                                                                                                                                                                 OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          PRICE APPLICATION 1939

PRICE APPLICATION NUMBER: US 08/496,632

FILING DATE: 29-UUN-1995

CLASSIFICATION MASER: US 08/548,368

PRICR APPLICATION DATA:

APPLICATION WINBER: US 08/548,368

FILING DATE: 01-NOV-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Anderson, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DCKET NUMBER: 2835-B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-044
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/670,354
FILING DATE: 25-JUN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US96-10895-6
; Sequence 6, Application PC/TUS9610895
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Immunex Corporation
51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 756822
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 291 amino acids
                                                                                                                        COMPUTER: Ploppy disk COMPUTER: Apple Macintosh OPERATING COMPUTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-670-354-6
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                         FILING DATE: 25 CLASSIFICATION:
                        Seattle
                                                                 USA
                                                               COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 KV 312
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Patent No. 6046310
GENERAL INFORMATION:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 GQVVCSIALFLYFRAQMDPNRISEDSTHC :YRILRLHENAGLQDSTLESEDTLPDSCRRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KELAELRESTSQMHTA----- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 KQAFQGAVQKELQHIVGPQRFSGAPAMME\SWLDVAQRGKPEAQPFAHLT--INAASIPS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 GSHKVTLSSWYHDRGWAKISNMTLSNGKL)!VNQDGFYYLYANICFRHHETSGSVPTDYLQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 99; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 LMVYVVKTSIKIPSSHNLMKGGSTKNWSGIJSEFHFYSINVGGFFKLRAGEEISIQVSNPS
               Sequence 2, Application US/08810453
Patent No. 585890
GENERAL INFORMATION:
APPLICANT: Walsh, Kenneth
TITLE OF INVENTION: FAS LIGAND C.)MPOSITIONS FOR TREATMENT OF
TITLE OF INVENTION: PROLIFERATIVE DISORDERS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 281;
                                                                                                                                                                     ADDRESSEE: Wolf, Greenfield & "acks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
CITY: Boston
                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DO:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DARA:
APPLICATION NUMBER: US/08/810,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 173.5; DB 2; 21.2%; Pred. No. 2.4e-09; tive 42; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: $1237,7004
TELECOMMUNICATION INFORMATION:
TELEPHONE: ($17)720-3500
TELEFAX: ($17)720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 PGVPHEGPLHPAPSAPAPAPPPAASR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 G-----MFQLFHLQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2, Application US/08815190A
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 343
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 281 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 21.28
Matches 67; Conservative
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266 LVNFEESQTFFGLYKL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-810-453-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                           STATE: MA
COUNTRY: US
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US-08-815-190A-2
US-08-810-453-2
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237 LMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPS 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 GQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT -- INAASIPS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 GSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQ 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 281;
APPLICANT: Outen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: INDEX COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,190A
FILING DATE: 11-MAR-1997
CLASSIFICATION NUMBER: US 08/614,584
FILING DATE: 13-MAR-1996
ATTONNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 173.5; DB 3; 21.2%; Pred. No. 2.4e-09; iive 42; Mismatches 108;
                                                                                                                                                                                           3: Townsend and Townsend and Crew LLF
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 011823-006710US TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
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amino acid
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Matches 67; Conservative
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MOLECULE TYPE: protein
US-08-815-190A-2
                                                                                                                                                                                                                                                San Francisco
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102 KEETKKENSF--EMQKGDQNPQIAAHV-----ISEASSKTTSVLQWAEKGYYTMSNNLV 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 -NLHEDFVFMKTIQRCNTGERSLSLL-----NCEEIKSQFEGFV-KDIM-----LN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--M 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 MKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
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                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                          APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                E: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/940,605A FILLING DATE: 04-SEP-1992 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-184-422-8; Sequence 8, Application US/08184422; Patent No. 556531; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME:
NAME:
REGISTRATION NUMBER: 18,875
REFERENCE/DOCKET NUMBER: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                     STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ARMITAGE, RICHARD APPLICANT: DAVISON, BARRY APPLICANT: FANSLOW, WILLIAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 261 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-940-605A-2
                       INFORMATION:
                                                                                                                                                                                                          New York
    Patent No. 5540926
                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                         GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KKELRKVAHLTGKSNSRSMP- 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPS 296
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-----KELAELRESTSQMHTA-----
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                Sequence 2, Application PC/TUS9500362
GENERAL INFORMATION:
APPLICANT: IMMUNEX CORPORATION
TITLE OF INVENTION: Ligand That Binds Fas Antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.4%; Score 173.5; DB 4; Best Local Similarity 21.2%; Pred. No. 2.4e-09; Matches 67; Conservative 42; Mismatches 108;
                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/179,138
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/190,559
FILING DATE: 01-FEB-1994
ATTOMNE: ANGENE ON FEBE-1994
ATTOMNE: ANGENE ON KATHLYON A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2805-WO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     омыЕR: PCT/US95/00362
06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 PGVPHEGPLHPAPSAPAPAPPAASR----
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                                                                                                       STREET: 51 University Street CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/07940605A
                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7
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amino acid
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LVNFEESQTFFGLYKL 281
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                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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PCT-US95-00362-2
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                                                                                                                                                                                                                         COUNTRY:
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WASHINGTON
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                           APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DEFECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT NUMBER: US/08/184,122
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REGISTRATION NUMBER: 34,693
REFERNCE/DOCKET NUMBER: 2810-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 2065870430
                                                                                                                                                                                                                                                                ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATLE
STATE: WASHINGTON
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
RENSHAW, BLAIR
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amino acid
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Sequence 2, Application US/08360923A Patent No. 5674492 GENERAL INFORMATION:
APPLICANT: ARMITAGE, RICHARD APPLICANT: FANSLOW, WILLIAM

US-08-360-923A-2

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92 LRLHE-----NAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFS 140
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MILLIAM
WENTION: METHOD OF PREVENTING OR TREATING
VENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
VENTION: EXPRESSING CD40
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
COMPUTER: Macinto
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Job time: 32935 sec
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NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
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Matches 75; Conservative
                                                                                      TITLE OF INVENTION: METTITLE OF INVENTION: DISSITITE OF INVENTION: EXPENDER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSEE: IMMUNEX COF
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MOLECULE TYPE: protein
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843 i Ell347 Human cDNA encoding F 924 i Ell354 Human cDNA encoding F 972 i Ull821 Human Fas ligand (Fas 1790 i A87645 Sequence 3 from Pate

1.3e-05 1.5e-05 1.5e-05 2.9e-05

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Ratio: 5.301
Percent Similarity: 100.000
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US-08-989-362-2 x AB008426
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                                                                                                                              seq_name: gb_ro:AB008426
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em_pat:E11347
em_pat:E11354
gb_pr6:HSU11821
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JOURNAL
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                       SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             764 | AB022036 Mus musculus DNA for d AB022037 Mus musculus DNA for d AB022037 Mus musculus DNA for d 1705 | U07059 Homo saptens Apo. 2 liga 1751 | AR012156 Sequence 1 from paten 1769 | U07518 Human TNF-related apopt 1366 | AR012157 Sequence 5 from paten 1366 | U37522 Mus musculus TNF-relate 1521 | AR012157 Sequence 3 from paten 1521 | AR012157 Sequence 3 from paten 1578 | AR012157 Sequence 1 from paten 1578 | AR012059 Homo saptens chromod 1678 | AC010059 Homo saptens chromod 1678 | AC010059 Homo saptens chromod 1678 | E11346 B Laurus mRNA for CD40 | 834 | E11349 Mouse CDNA encoding Fas 1623 | E11355 Mouse CDNA encoding Fas 157 | IU0984 Mus musculus CSTBL/6 Fa 1601 | S76752 Fas1=Fas 1igand finice, 1707 | IU06948 Mus musculus Fas 1igand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AB035138 Macaca fascicularis Cm
AB035139 Macaca mulatta Rm-Fasi
AB035140 Macaca nemestrina Pt-F
Ell156 cDNA encoding human Fas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AP013170 Mus musculus TNF-rela
AR02119 Sequence 6 from paten
RF053713 Mus musculus osteopro
AP019048 Mus musculus receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | AB032772 Mus musculus RANKL 3 m | AB037599 Homo saplens mRNA for | AF013171 Homo saplens TNF-rela | AB022039 Mus musculus DNA for | AC022297 Homo saplens clone | AL139382 Homo saplens chromc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U58995 Mus musculus strain Balk
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1 AB036798 Mus musculus mRNA
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                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Morinaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T.
Osteoclast differentiation factor is a ligand for
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                                                                                                                                                     osteoclast differentiation factor (ODF).
Mus musculus bone marrow stromal cells cell_line:ST2 cDNA to mRNA, clone_lib:pcDL-SRa296 clone:pOBM291.
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Submitted (22-OCT-1997) to the DDBJ/EMBL/GenBank databases.
Hisataka Yasuda, Snow Brand Milk Products Co., Ltd., Research
Institute of Life Science; 519 Shimo-Tshibashi, Ishibashi-machi,
Tochigi 329-05, Japan (E-mail:fvbd7042@mb.infoweb.or.jp,
Tel:0285-52-1331, Fax:0285-53-1314)
AB008426 951 bp mRNA ROD 02-MAY-1998 Mus musculus mRNA for osteoclast differentiation factor (ODF),
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 951)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998) 98188248
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1 267 C 248 9 205 L
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (11-JAN-2000) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology: 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)

Location/Qualifiers
1. 951
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 951)
                                                                                                                                            29-JUN-2000
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LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe
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LOCUS AB036798 951 bp mRNA ROD
DEFINITION MUS musculus mRNA for RANKL 1, complete cds.
ACCESSION AB036798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316
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Mus musculus
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RANKL 1.
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Ratio: 5.301
Percent Similarity: 100.000
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US-08-989-362-2 x AB036798
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\sf Chol}_1/{\tt Y} . The TRAF family of signal transducers mediates NF-kappaB activation
                                                                                                                                                                                                Wong, B.R., Josien, R., Lee, S.Y., Sauter, B., Li, H.L., Steinman, R.M and Choi, Y.
                                                                                                                                                                                                                                                       cytokine), a new TNF family member predominantly expressed in T cells, is a dendritic cell-specific survival factor J. Exp. Med. 186 (12), 2075-2080 (1997)
                                      Wong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M., Kalachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee,
                                                                         and Choi, Y.

TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
                                                                                                                                                                                                                                       TRANCE (tumor necrosis factor [TNF]-related activation-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wong, B.R., Josien, R., Lee, S.Y., Vologodskaia, M., Steinman, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wong, B.R., Rho, J., Arron, J., Lee, S.Y., Robinson, E. and Choi, Y. Direct Submission
Submitted (09-JUL-1997) Howard Hughes Medical Institue, The Rockefeller University, 1230 York Ave., New York, NY 10021, US. Location/Qualifiers
                                                                                                                                                                                                                                                                                                               3 (bases 1 to 2237)
Fuller K., Wong, B., Fox, S., Choi, Y. and Chambers, T.J.
TRANCE is necessary and sufficient for osteoblast-mediated activation of bone resorption in osteoclasts
J. Exp. Med. 188 (5), 997-1001 (1998)
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlaP 34
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Gaps: 0
Percent Identity: 100.000
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J. Biol. Chem. 273 (43), 28355-28359 (1998)
98447691
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/organism="Mus musculus'
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/chromosome="14"
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/product="TRANCE"
                      (bases 1 to 2237)
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Ratio: 5.301
Percent Similarity: 100.000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr
                                                                                                                                                                                                                                                                                                                                                            alGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 TIGGATGIGGCCCAGCGAGGCAAGCCIGAGGCCCAGCCATTIGCACACCT
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DEFINITION ACCESSION VERSION

KEYWORDS

ORGANISM

Sat

29-SEP-1999 357 84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117 117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134 20 67 roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe Percent Identity: 100.000 PAT Length: Gaps Osteoprotegerin binding proteins Patent: US 5843678-A 6 01-DEC-1998; Location/Qualifiers 1. .2295 to: 2295 DNA IS 5843678 /organism="unknown" 487 c 538 a from: 1 (bases 1 to 2295) Align seg 1/1 to: AR062119 Quality: 1675.00 Ratio: 5.301 Percent Similarity: 100.000 alignment_block: US-08-989-362-2 x AR062119 seq_documentation_block: LOCUS AR062119 Unclassified Boyle, W.J. 648 a Unknown Unknown alignment_scores source ORGANISM DEFINITION ACCESSION VERSION TITLE JOURNAL FEATURES BASE COUNT AUTHORS REFERENCE 258 51 809 34 29 358 508 151 KEYWORDS 101 167 SOURCE ORIGIN

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alignment_block:
US-08-989-362-2 x AF053713
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                                                                              ORIGIN
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Lacey, D.L. Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R., Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S., Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A., Qian, Y. -X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J., Delaney, J. and Boyle, W.,
Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation (2019) 9827661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AF053713 2299 bp mRNA ROD 09-MA
DEFINITION Mus musculus osteoprotegerin ligand mRNA, complete cds.
VERSION AF053713. GI:3057147
                                                                                                                                                                                                                                                                                                                                                                                                                                           1007
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                                                                                                                                                          217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspT
                                                                                                                                                                               SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe
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                                                                              SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl
                                                                                                                   758 AGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGC
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170. 1120
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STLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPE
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ICRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINV
GGFFKLMRAGEEISLQVSNPSCLAPDQDATYFGAFKVQDID"
494 c 541 g 623 t
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Gaps: 0
Percent Identity: 100.000
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                                              541 g
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                                                                                                         Ouality: 1675.00
Ratio: 5.301
Percent Similarity: 100.000
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Length: 316 Gaps: 0 Percent Identity: 99.684

to: 2225

from: 1

9

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LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                  287 CTGGCCCTCCTGGGGCTGGGACTGGGCCAGGTGTCTGCAGCATCGCTCT
                                                                                                                                                                                                                                              17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlaP
                                                                                                                                                                                                                                                                                                                        roSerAlaProAlaProProProAlaAlaSerArgSerMetPhe
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Quality: 1668.00
Ratio: 5.295
Harity: 99.684
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US-08-989-362-2 x AF019048
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ICFRHHATSGSVPTDYLKILMYYVYRTSIKIPSSHNLAMGGSTKNWSGNSEFHFYSINV
GGFFKLRAGEBISIOVSHPSLLDPDQDATYFGAFKVQDID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chorda;a; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodent.a; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2225)
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nuclear factor kappa B ligand
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Tometsko, M.E., Roux, E.R., "eepe, M.C., DuBose, R.F., Cosman, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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Direct Submission
Submitted (13-AUG-1997), Mo.; ecular Biology, Immunex Corp., University St., Seattle, Wiv 98101, USA
Location/Qualifiers
1., 2225
/organism="Mus municulus"
                                                                                                                                                             1020 CIGGIGAAGAAATTAGCATICAGGIGTCC/ACCCTICCCIGCIGGAICCG 1069
                                                                                                          284 laGlyGluGluIleSerIleGlnValSer/\snProSerLeuLeuAspPro 300
                                                                                       SerHisAsnLeuMetLysGlyGlySerTh: LysAsnTrpSerGlyAsnSe 267
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/db_xref="taxon:10090"
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/db_xref="GI:2612924"
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LOCUS
DEFINITION MUS musculus receptor activator (RANKL) mRNA, complete cds
ACCESSION AF019048
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137. .1087
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/gene="RANKL"
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336

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486
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                                                                                                487 GATGAAACAAGCCTTTCAGGGGGCCGTGCAGAAGGAACTGCAACACATTG
                                                                                                                                                                                                                                                                                            637 CACCATCAATGCTGCCAGCATCCCATCGGTTCCCATAAAGTCACTCTGT
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alignment_scores:

17

42

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uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlaP
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QMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQAFGGRVQKELQ
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RGWAKISNWTLSNGKERVNQDGFYYLFANICPRHHETSGSVPTDYLQLMVYVYKTSIR
IPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDDDQDAT
                                                                                                                                                                                                                                                       864 bp mRNA ROD 29-JUN-2000 ANNKL 2 mRNA for receptor activator of NF-kB ligand 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, pepartment of Pathology and Immunology; 1-5-45 Yushina, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Pax:81-3-5803-0123)
                                                                                                                                                                                                                                                                                                                                                                                                                Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                      284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
                                                                                                                                                     1037 GATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTTCAGGACATAGAC 1084
                                                                                                                                     301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
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Published Only in DataBase (2000) In press
2 (bases 1 to 864)
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/db_xref="taxon:10090"
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1 (bases 1 to 864)
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227 C
                                                                                                                                                                                                                                                                         Mus musculus RANKL
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Ratio: 5.163
Percent Similarity: 90.506
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                                                                                                                                                                                                                                                                                            complete cds.
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LOCUS AB032771
                                                                                                                                                                                                        seq_name: qb_ro:AB032771
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erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
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                 51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe
                                                                                                                                                                                         214 CAGGACTCGACTCTGGAGAGTGAAGACACACACTACCTGCAGCAGGAG
                                                                                                                                                                                                                                                                                                         SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl
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                                                                                                                                                                                                                                                                                                                                                                  AGCAACGGAAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGC
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NICFRHHETSGDLATEY.QLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSIN
VGGFFKLRSGEEISIEV NPSLLDPDQDATVFGAFKVRDID"
                                                                                                                                                    Eukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2201)
                                                                                                                                                                                                                            and
                   PRI 22-NOV-1997
nuclear factor kappa B ligand
                                                                                                                                                                                                                                                          A homologue of the TNF reciptor and its ligand enhance T-cell
                                                                                                                                                                                                     Anderson, D. M., Maraskovsky E., Billingsley, W.L., Dougall, W.C. Tometsko, M.E., Roux, E.R., 'Teepe, M.C., DuBose, R.F., Cosman, D.
                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nuclear factor kappa
                                                                                                                                                                                                                                                                                                                       Anderson, D.M., Billingsley W., Dougall, W., Maraskovsky, E., Cosman, D., Dubsoe, R. and G.Llibert, L.
Direct Submission
Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., University St., Seattle, W. 198101, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 GGCGGCCGCCGCCCCCCCCCCCCCCCCCCCCCCCCTCCATGTTC 275
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Percent Identity: 84.277
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Homo sapiens receptor actirator of
(RANKL) mRNA, complete cds.
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/db_xref="taxon:9;06"
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AF019047 1 GI:2612921
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/gene="RANKL"
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US-08-989-362-2 x AF019047
seq_documentation_block:
LOCUS AF019047
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09-MAY-1998
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1 (bases 1 to 2271)
Lacey_D.L., Timms_E., Tan, H.-L., Kelley_M.J., Dunstan, C.R.,
Burgess_T., Elliott, R., Colombero_A., Elliott, G., Scully, S., (disu, H., Sullivan, J., Hawkins, N., Davy_E., Capparelli, C., Eli, A., Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J., Delaney_J. and Boyle, W.J.
Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation
Cell 93 (2), 165-176 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPAA
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462 C

629 C
                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inc.,
                                                                                                                                                                                                                                                                                                                                                           98227661
2 (bases 1 to 2271)
Boylew.J. boliect Submission
Submitted (16-MAR-1998) Department of Cell Biology, Amgen, In
One Amgen Center Drive, Thousand Oaks, California 91320, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="regulates osteoclast differentiation and activation"
Homo sapiens osteoprotegerin ligand mRNA, complete cds {\rm AF05\,3712}
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Gaps: 2
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/db_xref="taxon:9606"
185. .1138
                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Ratio: 4.709
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AB032772 754 bp mRNA ROD 29-JUN-2000
Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                         481
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                                                                                                  erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu
             GlnAspSerThrLeuGluSerGluAspThr....LeuProAspSerCy
                                                               isIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly
                                                                                                                                                                    SerTrpLeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAl
                                                                                                                                                                                                                     hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet
                                                                                                                                                                                                                                                                                                                        832 GTATGCCAACATTTGCTTTCGACATCATGAAACTTCAGGAGACCTAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               hrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIle
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LOCUS AB032772
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Sat

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LOCUS AB037599
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TITLE
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                       379
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GFRKHRAGEELSHVSLLDPDQDATYFGAFKVQDID"

190 c 185 :1 170 t
                                                         expression
                                                                                                                                                       Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Keda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mil:toru.pth?@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81.3-5803-0123)
Mammalia; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae;
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                   1 (sites)
Iteda.T.. Takahashi,H. and Hirokawa,K.
Somatcostatin, a new marker of osteoblast, regulates the
of RANKL isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 ACACACTACCTGACTCCTGCAGGAGGATG/ AACAAGCCTTTCAGGGGGCC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 TCGGGTTCCCATAAAGTCACTCTGTCCTCTTGGTACCACGATCGAGGCTG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 uArgLeuHisGluAsnAlaGlyLeuGlnA: pSerThrLeuGluSerGluA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spThrLeuProAspSerCysArgArgMetI<sub>1</sub>ysGlnAlaPheGlnGlyAla 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValGlnLysGluLeuGlnHisIleValGlyProGlnArgPheSerGlyAl 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 aProAlaMetMetGluGlySerTrpLeuAspValAlaGlnArgGlyLysP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           roGluAlaGlnProPheAlaHisLeuThrlleAsnAlaAlaSerIlePro 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerGlySerHisLysValThrLeuSerSerTrpTyrHisAspArgGlyTr 192
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Percent Identity: 100.000
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2 (bases 1 to 754)
                                                                                                                                          Direct Submission
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Percent Similarity: 100.000
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US-08-989-362-2 x AB032772
                                                                                                                      Ikeda, T.
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                                  AUTHORS
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TITLE
JOURNAL
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                 REFERENCE
                                                                                      JOURNAL
                                                                                                        REFERENCE
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Nagal, M., Kyakumoto, S. and Sato, N.
Direct Submission
Submitted (26-JAN-2000) to the DDBJ/EMBL/GenBank databases.
Massarumi Nagal, Iwate Medical University School of Dentistry,
Department of Blochemistry: 19-1 Uchimaru, Morioka, Iwate 020 8505,
Japan (E-mail:mnagai@iwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436),
Fax:+81-19-654-4147)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomí;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOGE/trance; SODE/TRANCE.
Homo sapiens male tongue epithelial-like squamous cell cacinoma
cell_line:SCC-4 cDNA to mRNA.
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Cancer cells responsible for humoral hypercalcemia express mRNN
encoding a secreted form of ODF/TRANCE that induces osteoclast
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              275
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                                                                                                                                                                                                                    ThrSerGlySerValProThrAspTyrLeuGlnLeuMetValTyrValVa
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                                                                                                                                                                                                                                                                                                                       lnAspGlyPheTyrLeuTyrAlaAsnIleCysPheArqHisHisGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB037599 930 bp mRNA PRI
Homo sapiens mRNA for SODF/TRANCE, complete cds.
AB037599
                                                                                                                                                             1. .930
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95. .829
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BYLOLMYVYTKTSIKIPSSHTRAKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISI
BYLOLMYVYTKTSIKIPSSHTRID"
3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 PheGlnGlyAlaValGlnLysGluLeuGlnHisIleValGlyProGlnAr 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 CATCAGAGCAGAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 lnArgGlyLysProGluAlaGlnProPheAlaHisLeuThrIleAsnAla 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 AGAGGAGCAAGCTTGAAGCTCAGCCTTTTGCTCATCTCACTATTAATGCC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 AlaSerIleProSerGlySerHisLysValThrLeuSerSerTrpTyrHi 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 ACCGACATCCCATCTGGTTCCCATAAAGTGAGTCTGTCCTTGGTACCA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 sAspArgGlyTrpAlaLysIleSerAsnMetThrLeuSerAsnGlyLysL 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442 TGATCGGGGTTGGGCCAAGATCTCCAACATGACTTTTAGCAATGGAAAAC 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 etLysGlyGlySerThrLysAsnTrpSerGlyAsnSerGluPheHisPhe 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 TTTCAAGGAGCTGTGCAAAAGGAATTACAACATATCGTTGGATCACAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gIleLeuArgLeuHisGluAsnAlaGlyLeuGlnAspSerThrLeuGluS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222 ArgHisHisGluThrSerGlySerValProThrAspTyrLeuGlnLeuMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 tValTyrValValLysThrSerIleLysIleProSerSerHisAsnLeuM
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Gaps: 1
Percent Identity: 84.490
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                                                                                                                                                                                                                                                                               Quality: 1105.00
Ratio: 4.722
Percent Similarity: 95.510
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US-08-989-362-2 x AB037599
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                                                                                                                                                                   BASE COUNT
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1 (bases 1 to 1823)
Wong, B.R., Rho, J., Arron, J., Robinson, E., Orlinick, J., Chao, M.,
Kalachikov, S., Cayani, E., Bartlett, F.S. III, Frankel, W.N., Lee, S.Y.
                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1230 York Ave., New York, NY 10021, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells J. Biol. Chem. 272 (40), 25190-25194 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1823)
Wong, B. R., Rho, J., Arron, J., Lee, S.Y., Robinson, E. and Choi, Y. Direct Submission 1997) Howard Hughes Medical Institute, The Submitted (09-JUL-1997) Howard Hughes Medical Institute, The Rockefeller University, 1230 York Ave., New York, NY 10021, US 1.0calion/Qualifiers
                                                                                                                                                                                       AF013171 1823 bp mRNA PRI 19-SEP-1997
Homo sapiens TNF-related ligand TRANCE mRNA, partial cds.
AF013171
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domain"
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Percent Identity: 84.082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/map="13q14"
/cell_type="thymocyte"
1. 738
/note="encodes extracellular do
                                                                                                            826
                                                                      305 hrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="TNF-related ligand"
                                                                                             792 CATACTTTGGGGCTTTTTAAAGTTCGAGATATAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"TRANCE"
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Ratio: 4.705
Harity: 95.510
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                                                                                                                                               seq_name: gb_pr3:AF013171
                                                                                                                                                                                     seq_documentation_block:
LOCUS AF013171
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Percent Similarity:
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VERSION
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AUTHORS
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alignment_scores
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LOCUS AB022036S4 2029 bp DNA ROD 14-APR-2000
DEFINITION Mus musculus DNA for osteoclast differentiation factor, exon 5, ACCESSION AB022039
VERSION AB022039.1 GI:4127268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (sites)
Kodaira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N.,
Murakami,A., Ueda,M. and Hiŋashio,K.
Cloning and characterization of the gene encoding mouse
differentiation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordatı; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentiı; Sciurognathi; Muridae;
                            PheGlnGlyAlaValGlnLysGluLeuGlnHisIleValGlyProGlnAr 138
                                                                                                        201 CATCAGAGCAGAAAGCGATGGTGGATGGCTCATGGTTAGATCTGGCCA 250
                                                                                                                                                                                                                 AlaSerIleProSerGlySerHisLysVa)ThrLeuSerSerTrpTyrHi 188
                                                                                                                                                                                                                                                                                              301 ACCGACATCCCATTGGTTCCCATAAAGT(AGTCTGTCTTGGTACCA 350
                                                                                                                                                                                                                                                                                                                                                          251 AGAGGAGCAAGCTTGAAGCTCAGCCTTTTCCTCATCTCACTATTAATGCC 300
                                                                                                                                                                                                                                                                                                                                                                                                          221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgHisHisGluThrSerGlySerValPrcThrAspTyrLeuGlnLeuMe 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TyrSerIleAsnValGlyGlyPhePheLysLeuArgAlaGlyGluGluIl 288
51 AATTTTGAGACTCCATGAAAATGCAGATT!!TCAAGACACAACTCTGGAGA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tValTyrValValLysThrSerIleLysIleProSerSerHisAsnLeuM 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          etLysGlyGlySerThrLysAsnTrpSerGlyAsnSerGluPheHisPhe 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SASPArgGlyTrpAlaLysIleSerAsnMt tThrLeuSerAsnGlyLysL
                                                                                                                                                                                                                                                                                                                                                                                                       euArgValAsnGlnAspGlyPheTyrTyrIeuTyrAlaAsnIleCysPhe
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Submitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases. Kunihiko Kodaira, YS New Technology Institute Inc., Molecular Biology, Shimoushibashi 519, Ishibashi machi, Tochigi 329-0512, Japan (E-mall:YSNY@t-cnet.or.jp, Tel:81-285-52-2821, Fax:81-285-52-2821)
                                                                                                                                                                                                                 /db_xref="taxon:10090"
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join(AB022036.1:409. .630,AB022037.1:169. .330,
AB022038.1:146. .182,AB022038.1:274. .372,159. .580)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="osteoclast differentiation factor"
334 c 412 q 663 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 TCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTATGTCGTTAA 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 GGTTCCCATAAAGTCACTCTGTCCTTGGTACCACGATCGAGGCTGGGC 207
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                                                                                                                                                                                   /organism="Mus musculus"
    (1999)
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                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                   /strain="129
                                 (bases 1 to 2029)
                                                                                                                                                                                                                                                                                                                                                                                                                                 .1043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=5
                                                           Direct Submission
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US-08-989-362-2 x AB022036S4
                                                                                                                                                                        1. 2029
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Percent Similarity: 100.000
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    (1),
                                            Kodaira, K
Gene 230
99214075
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SOURCE

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NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                       2265 2364.239. Cont.9 12.24 bp in length 2365 6779: contig of 4415 bp in length 6780 6879; gap of 100 bp 6880 6879; gap of 100 bp 1332. Contig of 4453 bp in length 11333 11422; gap of 100 bp 1736 1735; contig of 5903 bp in length 1736 1736 23308; contig of 5873 bp in length 23309 23408; gap of 100 bp 28698; gap of 100 bp 28699; gap of 100 bp
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75674 75773: gap of 100 bp
75774 92375: contig of 16602 bp in length
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44529: contig of 8246 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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/note="assembly_fragment"
23042 c 23371 g 31675 t
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/note="assembly_fragment"
53773. 62948
/note="assembly_fragment
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63049. .75673
//note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
11433. .17335
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/note="assembly_fragment"
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/db_xref="taxon:9606"
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92476 113451; cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spiren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boquslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Kieln, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Kieln, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., McGurk, A., McKernan, K., McHonga, V., McCarthy, M., McKewan, P., McGurk, A., Mrada, C., Mlenga, V., Morrow, J., Naylor, J., Mihova, T., Mrada, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainnoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AC023297 113451 bp DNA HTG 03-MAR-2000
DEFINITION Homo sapiens clone RP11-21H9, WORKING DRAFT SEQUENCE, 13 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-FBB-2000) Whitehead Institute/MIT Center for Genome Submitted (11-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 3, 2000 this sequence version replaced gi:7139552.
All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: M13, M77815, 100% of reads

Sequencing vector: M13, M77815, 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 106493 bases at least 030

Consensus quality: 106791 bases at least 030

Consensus quality: 11178 bases at least 030

Consensus quality: 11178 bases at least 020

Insert size: 138000; agarose-fp

Insert size: 112251; sum-of-contigs

Quality coverage: 3.5 in 020 bases; sum-of-contigs
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-21H9
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                                                                                                                                                                                                                                                                                                                                                                                                                      AC023297.3 GI:7144965
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 113451)
                                                                                                               310 heLysValGlnAspileAsp 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
                                                                                                                                                                   558 TCAAAGTTCAGGACATAGAC 577
                                                                                                                                                                                                                         seq_name: gb_htg10:AC023297
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AUTHORS
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JOURNAL
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1200 others

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AL139382 205139 bp DNI,
DEFINITION Homo sapiens chromosome 13 clone RP11-86N24, *** SEQUENCING IN
PROGRESS ***, 27 unordered pieces.
                                                                                                                                                                                          209 InAspGlyPheTyrTyrLeuTyrAlaAsn::leCysPheArgHisHisGlu 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 lLysThrSerIleLysIleProSerSerH.:sAsnLeuMetLysGlyGlyS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 erThrLysAsnTrpSerGlyAsnSerGlu!heHisPheTyrSerIleAsn 275
                                                                                                                                                                       176 SerGlySerHisLysValThrLeuSerSerTrpTyrHisAspArgGlyTr 192
                                                                                                                                                                                                                                                                                                                                                                              226 ThrSerGlySerValProThrAspTyrLenGlnLeuMetValTyrValVa
                                                                                                                                          to: 113451
                                   Gaps: 0
Percent Identity: 90.071
                                                                                                                                       from: 1
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Center code: SC
Web Site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                       Align seg 1/1 to reverse of: AC02329"
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AL139382.4 GI:8978069
HTG; HTGS_PHASE1.
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                                                                                 alignment_block:
US-08-989-362-2 x AC023297/rev
              690.00
5.000
97.872
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                 Quality:
Ratio:
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                                              Percent Similarity
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alignment_scores
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KEYWORDS
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Project Infermation

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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 185877 bases at least 040
Consensus quality: 19731 bases at least 020
Consensus quality: 198268 bases at least 020
Insert size: 20739; sun-of-contigs
Insert size: 105413; 9.2% error; agarose-fp
Quality coverage: 3.00% in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106941 107040: gap of 100 bp 107040: gap of 107041 115418: contig of 8378 bp in length 115519 115518: gap of 100 bp 115519 11562: contig of 3644 bp in length 119163 119263: contig of 2049 bp in length 121312 121411: gap of 100 bp 121312 121411: gap of 100 bp 121312 129170: contig of 7559 bp in length 129171 129270: gap of 100 bp 129271 141607: contig of 12337 bp in length 129271 141607: contig of 12337 bp in length
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sporting of 1411 bp in length gap of 100 bp.
contig of 4353 bp in length
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19331 32371: contig of 13041 bp in length
32372 32471: gap of 100 bp
32472 34870: contig of 2399 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62661: gap of 100 bp 75173: contig of 12512 bp in length
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42014: contig of 7044 bp in length
42114: gap of 100 bp
50153: contig of 8039 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150: gap of 100 bp 62561: contig of 1211 bp in length
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89590: contig of 2205 bp in length
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5905 bp in length
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159553: contig of
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164333: contiq of
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Center project name: bA86N24
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182341 183761; conti
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188214: conti
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188215 188314: gap of
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Page 15

rth.												
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 lSerAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyA 309
                                                                                                                                               2625 others
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Ratio:
Percent Similarity:
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ORIGIN
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185.50 185.50 184.00 183.00

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/cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:103455
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Ratio: 5.301
Percent Similarity: 100.000
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calcium metabolism
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                                                                                                                                                                                                                                                                                                                                                                               Unidentified
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09-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-AUG-1997,
21-AUG-1997,
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                                                                                                              sed_name:
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.3e-14
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.1e-13
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1311.10
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     out_format : pfs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence Strd Orig 2Score EScore Len /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V69900 + /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:299965 +
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/cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V29519
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OM of: US-08-989-362-2 to: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                 Database: N_Geneseq_36:*
Database sequences: 480022
Database length: 187831343
Search time (sec): 72.480000
                                                                                                                                                                                                                                                                                                                                                                              Search information block:
Query: US-08-989-362-2
                                    Date: Dec 29, 2000 12:19
                                                                                                                           Command line parameters:
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                                                                                                                                                                                                                                                                                                                                           -WAIT -THREADS=1
                                                                       About: Results
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an osteoclastogenesis inhibitory factor (OCIF) binding molecule (OBM). The protein promotes and supports the separation and maturation of osteoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor form actor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay
                                                                                                                                                                                                                                                                                                                  Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM osteoclast; bone absorption factor; bone disorder; calcium metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence appears in the specification, which describes
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, Takahashi K, Tomoyas
i K, Yano K, Yasuda H;
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                                                                                                                                                                                                                                                     Nucleotide sequence of the specification.
                                       ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRAND MILK PROD CO LTD
                                       951
Sequence 951 BP; 231 A; 267 C;
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97JP-0097808.
97JP-0151434.
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97JP-0224803
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Washida N, Yamaguchi
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Length: 316 Gaps: 0 Percent Identity: 100.000

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GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117 alGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150 500 550 900 450 167 184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200 700 850 SerHisAsnLeuMetLysGlyGlySerThr.ysAsnTrpSerGlyAsnSe 267 20 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlr ValValCysSerIleAlaLe 67 uPheLeuTyrPheArgAlaGlnMetAspP:oAsnArgIleSerGluAspS 84 roSerAlaProAlaProAlaProProPro/laAlaSerArgSerMetPhe rGluPheHisPheTyrSerIleAsnValGl GlyPhePheLysLeuArgA LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe aAsnIleCysPheArgHisHisGluThrSe:GlySerValProThrAspT yrLeuGlnLeuMetValTyrValValLysTirSerIleLysIleProSer from: 1 to: 951 Align seg 1/1 to: V69900 US-08-989-362-2 x V69900 alignment_block: 101 151 17 51 34 201 401 451 234 267 51 29 151 167 251

134

501 184 201

601

551

217

651

701

801

101

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The present sequence encodes a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of poly activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other
                                                                                                                                                                                                                                                                                                                 Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In vivo down-regulation of osteoprotegerin ligand (OPGL) activity to treat, prevent and ameliorate osteoporosis ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases or conditions characterised by excessive bone resorption
laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
                                CTGGTGAAGAAATTAGCATTCAGGTGTCCAACCCTTCCCTGCTGGATCCG 900
                                                               seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT: 299965
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                                                                                                                                                                                                                                                                                      a murine osteoprotegerin ligand (OPGL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/product= "osteoprotegerin ligand"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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ID Z99965 standard; DNA; 951
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                                                                                                                                                                                                                                                                                      DNA encoding
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284
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316 0

Length: Gaps:

Quality: 1675.00 Ratio: 5.301

alignment_scores:

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                                                                                                                                                                                                                                                                                                                                                                                                                                             gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
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                                                                                                                                                                                                                                                                                          84
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                                                                                                                                                                                                                                                                                                     rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA
                                                                                                                                    17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlaP
                                                                                                                                                                                       roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe
                                                                                                                                                                                                                                      51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe
                                                                                                                                                                                                                                                    uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS
                                                                                                                                                                                                                                                                                                                                           erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                          GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr
                                                                                                                                                                                                                                                                                                                                                                                                        erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 CCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe
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                                                             from: 1
Percent Similarity: 100.000
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US-08-989-362-2 x Z99965
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This sequence encodes the osteoclast formation promoting factor (OBM). The invention relates to an OBM binding protein (OBM-BP). The protein is useful as a preventive and/or treating agent for bone metabolic diseases such as osteoporosis. Substances which inhibit the binding of OBM to OBM-BP can be used as biochemical reagents.
                                                                                                                                                                                                                                                                                    promoting factor;
                          laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
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                                                                                316
                                                                                                                                  seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:Z49024
TGAATTCCACTTTTATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAG
                                        uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlaP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osteoclast formation promoting factor coding sequence
                                                                              901 GATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTTCAGGACATAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 316
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                  OBM-BP; OBM binding protein; osteoclast formation bone metabolic disease; osteoporosis; therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             new protein, a DNA and its application
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Ratio: 5.301
Percent Similarity: 100.000
                                                                                                                                                            seq_documentation_block:
ID Z49024 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: 249024
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US-08-989-362-2 x Z49024
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                                                                                                                                                                                                                                                                                                                                                   JP11332581-A
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Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM, osteoclast; bone absorption factor; bone disorder; calcium metabolism;

Location/Qualifiers 125..1075 /*tag= a

WO9846644-A1

22-OCT-1998. 15-APR-1998;

Unidentified

Key

an OCIF-binding molecule (OBM)

encoding

acid

Nucleic

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400
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                                                                      erThrHisCysPheTyrArglleLeuArgleuHisGluAsnAlaGlyLeu 100
                                                                                                           GlnAspSerThrLeuGluSerGluAspThiLeuProAspSerCysArgAr 117
                                                                                                                                                                                                                                                                                                                                                                                                                             ATCTTCAGCTGATGGTGTATGTCGTTAAAACCAGCATCAAAATCCCAAGT 750
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                                 67 uPheLeuTyrPheArgAlaGlnMetAspPyoAsnArgIleSerGluAspS 84
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspGlnAspAlaThrTyrPheGlyAlaPhelysValGlnAspIleAsp 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V69886
LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe
                                                                                                                                                        SerAsnGlyLysLeuArgValAsnGlnAsp3lyPheTyrTyrLeuTyrAl
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The present sequence encodes an ostcoclastogenesis inhibitory factor separation and maturation of ostcoclasts in the presence of bone absorption factors such as calcitriol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (SOBM) which is a shorter chain. OBM may be used for screening potential inhibitors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of disorders of bone function and calcium metabolism. The antibodies can be used for assay of the protein.

G; 359 T; 0 other;

Sequence 1538 BP; 382 A; 381 C; 416

components of drugs.

Length: 316 Gaps: 0 Percent Identity: 100.000

Quality: 1675.00 Ratio: 5.301 Percent Similarity: 100.000

alignment_scores

Protein binding to osteoclastogenesis inhibitory factor - useful for, e.g. treatment and investigation of disorders of bone and calcium metabolism

9; Pages 108-109; 151pp; Japanese.

Claim

Morinaga T Tsuda E;

Goto M, Higashio K, Kinosaki M, Kobayashi F, Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Washida N, Yamaguchi K, Yano K, Yasuda H;

WPI; 1998-594563/50.

(SNOW) SNOW BRAND MILK PROD CO LTD.

98WO-JP01728. 97JP-0332241. 97JP-0097808. 97JP-0151434. 97JP-0217897.

> 15-APR-1997; 09-JUN-1997; 12-AUG-1997; 21-AUG-1997;

97JP-0224803

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17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
                                             Align seg 1/1 to: V69886 from: 1 to: 1538
alignment_block:
US-08-989-362-2 x V69886
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BP

seq_documentation_block:
ID V69886 standard; cDNA to mRNA; 1538

(first entry)

10-FEB-1999

V69886;

HX SX H

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us-08-989-362-2.rng

ВР

/41489 standard; cDNA; 2191

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                                               225 CTTCTGCACCGGCTCCGGCGCCGCCGCCGCCGCTCCCGCTCCATGTTC
                                                                                              51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe
                                                                                                                                                                                                                              erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu
                                                                                                                                                                                                                                               101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr
                                                                                                                                                                                                                                                                                                               gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              525 TGGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGG
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                              34 roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe
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Align seg 1/1 seq_name: /cgn2_2/gcgdata/geneseq/genesegn/NA1998.DAT:V41489

seq_documentation_block

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The Hericus of the invention of the degree protein is expressed highly on polarised Th1 T cells, binding of 499E9 protein is expressed highly on polarised Th1 T cells, binding of 499E9 to its receptor may result in either immune cell expansion or apoptosis. Antegonists of 499E9 may be used to modulate immune responses in abnormal situations, e.g. autoimmune disorders including rheumatoid arthritis, systemic lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as acute inflammatory responses in which T cell expansion, activation or immunological T-cell memory play an important role. The antibodies can be used to raise anti-idiotypic antibodies which will be useful in detecting or diagnosing various immunological conditions related to the expression of antigens of 499E9. The antibodies, and fragments of 499E9 can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse cell surface antigen, 499E9 protein - used to treat conditions associated with abnormal physiology or development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is is the nucleotide sequence encoding the mouse 499E9 protein, uthe method of the invention to treat conditions associated with
                                                                                                                                protein; polarised Th1 T cell; immune cell; apoptosis;
                                                                                                                                             antagonist; autoimmune disorder; rheumatoid arthritis; systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis; acute inflammatory response; antibody; antigen; cancer; ss.
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Gaps: 0
Percent Identity: 100.000
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125..1072
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                                                                                               of mouse 499E9
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Percent Similarity: 100.000
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US-08-989-362-2 x V41489
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P-PSDB; W59654.
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                                      roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe
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                                                                                     425 CAGGACTCGACTCTGGAGAGTGAAGACACICTACCTGACTCCTGCAGGAG
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The present sequence encodes murine TNP-related activation induced cytokines (TRANCE). Human or murine TRANCE polypeptides or their variants, fargments, derivatives or analogues may be used as modulators of immune response in a mammal comprising, antisense sequences to TRANCE and fusion proteins comprising human and/or murine TRANCE. Agonists and antagonists of TRANCE, can be used to modulate immune response by increasing or decreasing the life span of mature dendritic cells and increasing or decreasing to eall activation. These techniques are especially useful for treating immune system related conditions such as HIV, cannot an autoimmune disease or hypersensitivity to an allergen. The TRANCE polypeptides can be used to increase the viability of dendritic cells in vivo or in vitro, especially when used in conjunction with proteins of the tumour necrosis factor (TNF) superfamily (especially
                                                                                                                                                                      TRANCE; tumour necrosis factor superfamily; signal transduction; TNF; TNF-related activation induced cytokine; immune response; cancer; autoimmune disease; HIV; hypersensitivity; allergen; ds.
seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:X80224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer
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97US-0989479.
98US-0034099.
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                                                                                                                                         Murine TRANCE encoding cDNA.
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                                             X80224 standard; cDNA;
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                              seq_documentation_block:
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                                                                                                                                       uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS
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The present sequence encodes human osteoprotegerin (OPG) binding protein Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein. OPG binding protein is used in binding assays to determine Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor; osteoprotegrin (OG) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including intracellular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that modulate binding of OPG binding protein to osteoclast differentiation and activation receptor (OBAR). The nucleic acid molecule encoding OPG binding protein can be used to detect OPG binding protein-encoding sequences, e.g. screening for related sequences, also to produce transgenic animal models, while complementary sequences are used for Human osteoprotegerin binding protein encoding DNA from the 32D-F3 ins antisense regulation of OPG binding protein expression. Modulators of OPG binding protein, particularly soluble forms of OPG binding protein, or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, optionally in combination with agents that promote bone growth. Nucleic acid encoding osteoprotegrin binding protein \cdot useful for, e.g. treating bone diseases by modulating osteoclast differentiation and for diagnosis "osteoprotegerin binding protein" seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V70284 BP; 648 A; 487 C; 538 G; 622 T; 0 other; Length: 316 Gaps: 0 Percent Identity: 100.000 Location/Qualifiers 158..1108 ВР Claim 1; Fig 1; 47pp; English. 98US-0052521. 97US-0842842. 97US-0880855. 98WO-US07584 /product= ^ V70284 standard; DNA; 2295 (first entry) Quality: 1675.00 Ratio: 5.301 Percent Similarity: 100.000 Paget's disease; ss. WPI; 1998-594578/50. seq_documentation_block: (AMGE-) AMGEN INC P-PSDB; W83194 Sequence 2295 sapiens W09846751-A1 alignment_scores: 15-APR-1998; 30-MAR-1998; 16-APR-1997; 11-FEB-1999 23-JUN-1997; 22-OCT-1998 Boyle WJ; Homo

507 200 217 307 407 erThrHisCysPheTyrArgIleLeuArgIeuHisGluAsnAlaGlyLeu 100 457 GlnAspSerThrLeuGluSerGluAspThiLeuProAspSerCysArgAr 117 134 607 167 657 184 707 807 957 257 20 29 84 34 uMetGlySerGlyProGlyValProHisGiuGlyProLeuHisProAlaP gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 1 MetArgArgAlaSerArgAspTyrGlyLy: TyrLeuArgSerSerGluGl uPheLeuTyrPheArgAlaGlnMetAspP1oAsnArgIleSerGluAspS alGlyProGlnArgPheSerGlyAlaPro/laMetMetGluGlySerTrp yrLeuGlnLeuMetValTyrValValLysThrSerIleLysIleProSer SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspT to: 2295 from: 1 to: V70284 alignment_block: US-08-989-362-2 x V70284 Align seg 1/1 ¢ 208 158 17 308 29 458 208 558 151 608 658 708 758 217 828 5 358 84 108 101 117 134 167 184 808 234 251 908 267 958 201

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The present sequence encodes a murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the in vivo down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL polypeptide or induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nsed
                                                                                                                                                                                                                                                                                                     Osteoprotegerin ligand, OPGL, osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption; ss.
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             laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
                                                         seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:299966
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/product= "osteoprotegerin ligand"
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170..1120
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ID Z99966 standard; DNA;
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Gaps: 0
Percent Identity: 100.000
                                                                                                    to: 2299
                                                                                                  from: 1
Ratio: 5.301
Percent Similarity: 100.000
                                                                                                 Align seg 1/1 to: Z99966
                                                alignment_block:
US-08-989-362-2 x Z99966
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immune or inflammatory response. Inhibition of NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This cDNA encodes a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
                                                                                                                                                                                                                                                                                                                                                                                                                  necrosis factor-kappa B; NF-kB; receptor activator; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
                   970 TGAATTCCACTTTTATTCCATAAATGTTGGGGGATTTTTCAAGCTCCGAG 1019
                                                                                         1020 CIGGIGAAGAAATIAGCATICAGGIGICCAACCCIICCCIGCIGGAICCG 1069
                                                                                                                                                                                                                                                                                                                                                                               NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
                                                    284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
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/product= "murine RANKL (ligand for RANK)"
                                                                                                                                                1070 GATCAAGATGCGACGTACTTTGGGGCTTTCAAAGTTCAGGACATAGAC 1117
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96US-0059978.
97US-0813509.
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P-PSDB; W69956.
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07-MAR-1997;
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from the negative effects of chem therapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
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                                                                                                                                                                                                                               3 GGCGTCCCACACGAGGGTCCGCTGCACCCCCGCCCTTCTGCACCGGCTCC
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Percent Identity: 99.660
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                                                                                                  Quality: 1554.00
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US-08-989-362-2 x V41377
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This cDNA encodes a murine RANKL, a ligand for the RANK (receptor activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK with binds to RANK igand (RANKL). The soluble RANK with a soluble RANK which binds to used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK and personse that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                      RANK; necrosis factor-kappa B; NF-kB; receptor activator; human; immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                        NF-kB receptor activator RANK ligand (RANKL) encoding cDNA
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                                                                                                                                                                                                                                                        seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V41371
                                                           ysGlyGlySerThrLysAsnTrpSerGlyAsnSerGluPheHisPheTyr
                                                                                                                               rlleGlnValSerAsnProSerLeuLeuAspProAspGlnAspAlaThrT
                                                                                                                                            703 AAGGAGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCCACTTTTAT
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96US-0059978.
97US-0813509.
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inflammatory reactions. They can also be used in adjunct therapy disease characterised by neoplastic cells that express RANK. The can also be used for detection and drug screening.
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                                                        Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;
                                                                                                                           Gaps: 0
Percent Identity: 99.660
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activator of necrosis factor wappab (NF-KB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK may be used for inhibiting activation of NF-KB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-KB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated ligand for receptor activator of NF-kappa B - used to develop products for augmenting an immune response for inhibiting an inflammatory response and for protection of cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
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                                                                                                                                                                                                                                                                              seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V41378
703 AAGGAGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCCACTTTTAT
                                                                                     rIleGlnValSerAsnProSerLeuLeuAspProAspGlnAspAlaThrT
                                                                                                                                                          803 CATTCAGGTGTCCAACCCTTCCCTGCTGGATCCGGATCAAGATGCGACGT
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ID V41378 standard; cDNA; 954
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shock or sepsis, graft-versus-hos: reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATATCGTTGGATCACAGCACATCAGAGCA;AGAAAGCGATGGTGGATGGC 447
                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
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                                                                                                                                                                                                                                                                                                                                                    1 MetArgArgAlaSerArgAspTyrGlyLy; TyrLeuArgSerSerGluGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlaP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGl NValValCysSerIleAlaLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uPheLeuTyrPheArgAlaGlnMetAspP:oAsnArgIleSerGluAspS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrLeuSerAsnGlyLysLeuArgValAs \GlnAspGlyPheTyrLe
                                                                                                                                                 other;
                                                                                                                                                                                                          Length: 318
Gaps: 2
Percent Identity: 84.277
                                                                                                                                                                                                                                                                                                                                                                                                                                    GATGGCGCCCCCGGACCCCCGCACGAGGCCCCCTGCACGAGGCCCCCTGCAC
                                                                                                                                              BP; 255 A; 239 C; 227 G; 233 T; 0
                                                                                                                                                                                                                                                                                                                        to: 954
                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                         Quality: 1417.50
Ratio: 4.709
Percent Similarity: 94.654
                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: V41378
                                                                                                                                                                                                                                                                        alignment_block:
US-08-989-362-2 x V41378
                                                                                                                                              Sequence 954
                                                                                                                                                                                               alignment_scores:
                                                                                                                screening
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- useful
                                                                                                                                                                                                                                                                                                                                                                              factor-kappa B; NF-kB; receptor activator; human;
                                                                                                                                                                                                                                                                                                                                                                                       immune response; inflammatory response; toxic shock; sepsis; RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
                                                                                                                                   847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                        747
                                                                                                                                                                                                                                                                                                                                                           receptor activator RANK ligand (RANKL) encoding cDNA.
                                                                                               797
                                                                                                                                                                                                               947
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "human RANKL (ligand for RANK)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated receptor activator of necrosis factor-kappa for, e.g. developing products for regulating an immune or inflammatory response, treating toxic shock or sepsis
                                                                                                                                                                                                                                                                      seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V41372
                                    uTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValProT
          AspProAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIl
                                                                                                                yAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPheDysL
                                                                                                                                                       euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maraskovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7; Pages 59-60; 80pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                   ВР
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V41372 standard; cDNA; 954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
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                                                                                                                                                                                                                                                                                                                                                                               necrosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson DM,
                                                                                                                                                                                                                                 eAsp 316
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09828424-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1996;
07-MAR-1997;
                                                                                                                                                                                                                                                   AGAT 951
                                                                                                                                                                                                                                                                                                                                        08-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                           NF-kB
                                                                                                                                                                                                                                                                                                                                                                              RANK;
                  648
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                                                                                                                265
                                                                                                                                   798
                                                                                                                                                      282
                                                                                                                                                                                           299
                                                                                                                                                                                                              868
                                                                                                                                                                                                                                 315
                                                                                                                                                                                                                                                    948
                                    232
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activator of necrosis factor (TNF) family. Host cells transformed or transfected with an expression vector comprising the RANK encoding nucleic acid can be used to produce recombinant RANK protein. The soluble RANK may be used for inhibiting activation of NF-kB, by contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to RANK ligand (RANKL). The soluble RANK with a soluble RANK which binds to BANK ligand (RANKL). The soluble RANK with a soluble RANK which binds to NF-kB by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response. Inhibition of NF-kB by RANK antagonist may be useful in ameliorating of RANK, e.g. in treating toxic shock or sepsis, grafit-versus-host reactions, or acute inflammatory reactions. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. The products
                        cDNA encodes a human RANKL, a ligand for the RANK (receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aHisLeuThrIleAsnAlaAlaSerIleProSerGlySerHisLysValT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 GTGGCCCTCCTGGGGCTGGGGCTGGGCCAGGTTGTCTGCAGCGTCGCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 GCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 isIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerTrpLeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GlnAspSerThrLeuGluSerGluAspThr....LeuProAspSerCy
                                                                                                                                                                                                                                                                                                                                                                     G; 233 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 318
Gaps: 2
Percent Identity: 84.277
                                                                                                                                                                                                                                                                                                                        can also be used for detection and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 954
                                                                                                                                                                                                                                                                                                                                                                     255 A; 239 C; 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
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Ratio: 4.709
Percent Similarity: 94.654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-989-362-2 x V41372
                                                                                                                                                                                                                                                                                                                                                                     Sequence 954 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
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Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator;
                                                                           232
                                                                                                                                                       265
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                                       215
                   597
                                                                                             697
                                                                                                                                   747
                                                                                                                                                                         797
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                                                                                                                                                                                                               847
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                                                                                                                                                                                                                                                     897
                                                                                                                                                                                                                                                                                            947
                                                                                                                                                                                           199 ThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLe
                                                                           215 uTyrAlaAsnIleCysPheArgHisHisGluThrSerGlySerValProT
                                                                                                                          ProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGl
                                                                                                                                                                                                                                  euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu
                                                                                                                                                                                                                                                                        seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:Z99964
                                                hrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIle
                                                                                                                                                                 DNA encoding a human osteoprotegerin ligand (OPGL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune response; osteoporosis; bone resorption; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "osteoprotegerin ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
185..1138
                                                                                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-DK00481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0102896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98DK-0001164
                                                                                                                                                                                                                                                                                                                                                                                 Z99964 standard; DNA; 2271
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haaning J;
                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200015807-A1
                                                                                                                                                                                                                                                                                                              eAsp 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3-SEP-1999;
                                                                                                                                                                                                                                                                                                                                 948 AGAT 951
                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halkier T,
                                                                                                                                                                                                                                                                                                                                                                                                     299964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
 182
                  548
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632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a human osteoprotegerin ligand (OPGL).

Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthisised as a type II transmembrane protein. The murine and human OPG, polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1.

It is not capable of inducing ostroclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method Storm regulation of OPGL activity in an animal. The mithod comprises using at least one OPGL polypeptide or subsequence, and/o: at least one OPGL analogue to induce in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other calseases or conditions characterised by excessive bone resorption.
                                                      In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnAspSerThrLeuGluSerGluAspThr....LeuProAspSerCy 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerTrpLeuAspValAlaGlnArgGlyLys?roGluAlaGlnProPheAl 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 ATGCGCCGCCCAGCAGACTACACCAAGTACCTGCGTGGCTCGGAGGA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2271 BP; 658 A; 462 C; 5:12 G; 629 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 318
Gaps: 2
Percent Identity: 84.277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treat, prevent and ameliorate osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tc.: 2271
                                                                                                              Disclosure; Page 75-77; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 1417.50
Ratio: 4.709
Percent Similarity: 94.654
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US-08-989-362-2 x 299964
2000-271444/23
                 P-PSDB; Y84417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores
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Human; osteoprotegerin binding protein; OPG binding protein; arthritis; osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR; hypercalcaemia; osteoclast differentiation and activation receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.11nsert.
                                                                                                                                                                                                                                                                                                                                                                                                             1031
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hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet
                                                                                                                                                    aHisLeuThrIleAsnAlaAlaSerIleProSerGlySerHisLysValT
                                                                                                               uTyrAlaAsnIleCysPheArgHisHisGluThrSerGlySerValProT
                                                                                                                                                                                                                                                                     hrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIle
                                                                                                                                                                                                                                                                                   ProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGl
                                                                                                                                                                                                                                                                                                                                                                                yAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysL
                                                                                                                                                                                                                                                                                                                                                                                                                                       euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu
                                                                                                                                                                                                                                                                                                                                                    CCAAGTTCTCATACCCTGATGAAAGGAGGAAGCACCAAGTATTGGTCAGG
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185..1138
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ID V70285 standard; DNA; 2274
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Host cells transfected with vectors containing nucleic acid molecules encoding OPG binding protein are used to produce recombinant OPG binding protein is used in binding assays to determine osteoprotegrin (OC) in biological samples; to screen for specific binding agents (particularly agonists and antagonists, including cartecillular proteins); to raise Ab (useful in immunoassays for detection of OPG binding protein) and to identify compounds that and activation receptor (ODAR). The nucleic acid molecule encoding OPG binding protein and activation receptor (ODAR). The nucleic acid molecule encoding oPG binding protein can be used to detect OPG binding protein-encoding can activation receptor (ODAR). The nucleic acid molecule encoding oPG binding protein can be used to detect OPG binding protein-encoding calculations of opf binding protein, while complementary sequences are used for antisense regulation of OPG binding protein expression. Modulators of OPG binding protein particularly soluble forms of OPG binding protein can be used to treat or prevent bone diseases, e.g. osteoporosis, bone loss caused by arthritis or metastases, hypercalcaemia, Paget's disease, periodontal disease, osteoporosis, loosening of prostheses, continually in combination with agents that promote bone growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes human osteoprotegerin (OPG) binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid encoding osteoprotegrin binding protein - useful for,
e.g. treating bone diseases by modulating osteoclast differentiation
and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 4; 47pp; English.
97US-0842842
97US-0880855
                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-594578/50
                                                                                                                                                       (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W83195
                                                    23-JUN-1997;
16-APR-1997;
                                                                                                                                                                                                                                                     Boyle WJ;
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Length: 318 Gaps: 2 Percent Identity: 84.277 Quality: 1417.50 Ratio: 4.709 Percent Similarity: 94.654 US-08-989-362-2 x V70285 alignment_scores: alignment_block

to: 2274 from: 1 Align seg 1/1 to: V70285

1 MetArgArgAlaSerArgAspTyrGlyLysTyrLeuArgSerSerGluGl 17

34 17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlaP

34 roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe

382 84

uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS

29

84

erThrHisCysPheryrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100 ::|||||||||||||||| :::|
GCACTCACTGCATTTATAGAATTTTGAGACTCCATGAAAATGCAGATTTT 481 432

Homo sapiens

human;

148 215 265 282 1032 TACGGTCTGGAGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACTG 1081 731 232 982 GAATTCTGAATTCCATTTTTATTCCATAAACGTTGGTGGATTTTTTAAGT 1031 115 132 581 631 SerTrpLeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAl 165 681 aHisLeuThrIleAsnAlaAlaSerIleProSerGlySerHisLysValT 182 198 831 881 248 931 981 Nucleic acid encoding a human OCIF-binding molecule (OBM) GlnAspSerThrLeuGluSerGluAspThr....LeuProAspSerCy sArgArgMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnH 215 uTyrAlaAsnIleCysPheArgHisHisGluThrSerGlySerValProT hrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIle ProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGl 282 euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu 482 CAAGACACACTCTGGAGAGTCAAGATACAAAATTAATACCTGATTCATG hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet ThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLe 265 yAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysL seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V69887 isIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly BP. 954 V69887 standard; cDNA to mRNA; (first entry) seq_documentation_block: 1132 AGAT 1135 315 eAsp 316 10-FEB-1999 232 132 149 632 165 682 182 732 199 782 882 249 101 115 832

Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM; osteoclast; bone absorption factor; bone disorder; calcium metabolism;

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GTGGCCCTCCTGGGGCTGGGCCAGGTTGTCTGCAGCGTCGCCCT
                                                      uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS
     148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes an osteoclastogenesis inhibitory factor (OCIF)-binding molecule (OBM). The protein promotes and supports the absoration and maturation of osteoclasts in the presence of bone absorption factors such as calcitiol or parathyroid hormone (PTH). OBM is isolated from stroma cells cultured in the presence of a bone absorption factor by separation and solubilisation of membrane proteins then affinity chromatography using OCIF. It exists in a full-sequence form and a solubilised form (sOBM) which is a shorter chain. OBM may be used for screening potential inhititors and modifiers of its biological activity, and screening for receptors to OBM which mediate its function. These substances can then be used in the treatment of discorders of bone function and calcium metabolism. The antibodies can be used for assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, for investigative and diagnostic purposes, and as
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for, e.g. treatment and investigation of disorders of bone and
calcium metabolism
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Tsuda E;
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Washida N, Yamaguchi K, Yano K, Yasuda H;
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Gaps: 2
Percent Identity: 83.962
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kobayashi F,
                                                                                                                                                                                                                                                                                                                                                                                                    (SNOW ) SNOW BRAND MILK PROD CO L'D
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Location/Qualifie.s
1..954
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinosaki M,
                                                                                                                                                                                                                                                                        97JP-0097808.
97JP-0151434.
97JP-0217897.
97JP-0224803.
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Ratio: 4.698
Percent Similarity: 94.340
                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goto M, Higashio K,
Nakagawa N, Shima N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-989-362-2 x V69887
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                                                                                                                                                                                                  15-APR-1998;
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09-JUN-1997
                                                                                                                                                                                                                                                                                                                         12-AUG-1997
21-AUG-1997
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CGCCGCCGCCGCCCGCACCACCCGCGCCCCCCGCCCCCAGGTTC 147

LeuAlaLeuLeuGlyLeuGlyCln'/alValCysSerIleAlaLe

51

34 roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe

20

29

51

from: 1 to: 954

Align seg 1/1 to: V69887

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347
                                                                            isIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly 148
                                                                                                                                      447
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                                                                                                                                                        SerTrpLeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAl
                                                                                                                                                                                                                                                                                                                                                              299 AspProAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIl
          101 GlnAspSerThrLeuGluSerGluAspThr....LeuProAspSerCy
                                                                                                                                                                   199 ThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLe
                                                                                                                                                                                                                                                                                   hrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIle
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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 protein search, using sw model OM protein

; Search time 412.16 Seconds 2000, 19:33:49 December 28, Run on:

(without alignments)
48.654 Million cell updates/sec

US-08-989-362-2

1 MRRASRDYGKYLRSSEEMGS.....LLDPDQDATYFGAFKVQDID Perfect score: Sednence:

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

182106 Total number of hits satisfying chosen parameters:

182106 seqs, 63460219 residues

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

- rat CD40 ligand - huma CD40 ligand - mous tumor necrosis fac hypothetical prote TipC protein - sli tumor necrosis fac tumor necrosis fac CD40 ligand - bovi - human necrosis fac tumor necrosis fac hypothetical prote glyceraldehyde-3-p lypothetical prote .ymphotoxin-beta -.ymphotoxin beta necrosis necrosis necrosis necrosis fas ligand -Fas ligand -Description Fas ligand tumor tumor tumor Lumor SUMMARIES OWMSN \$22052 JH0529 \$11688 QWHUN A25451 154490 S24642 S52715 S12606 JU0029 I49139 S53090 A49266 A53062 I38707 A46066 S06192 S49742 T17414 T23649 I49681 S38114 B55514 B40333 JQ1344 DB Match Length **644**6010007700011008760 185.5 183 173.5 171.5 145 146.5 144.6 141.6 143.5 137.5 133. Score Result

tumor necrosis fac	secreted klotho pr	hypothetical prote	membrane klotho pr	serine/threonine-s	genome polyprotein	sialoadhesin - mou	tumor necrosis fac	adenylyl cyclase-a	hypothetical 176K	hypothetical prote	probable 60K inner	probable cytoskele	microtubule-associ	tryptophan synthas	hypothetical prote
JH0309	JC5926	T23456	JC5925	T39500	S40770	S50065	B27303	I38409	9600ÖC	H75253	JQ1221	T37781	A43359	T01088	T36149
_	7	7	7	7	Н	~	-	7	7	7	-	7	7	7	N
197	549	785	1012	658	3011	1694	202	477	1547	347	260	1420	2774	275	451
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92.5 5.5	92 5.	92 5	92 5	90.5 5	90	68	88.5	88.5	88.5	88	88	88	88	87	87

ALIGNMENTS

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15;
                                                             C; Species: Bos primigenius taurus (cattle)
C; Jacesion: S53090
R; Martens, B.E.L.C.; Muriuki, M.
Submitted to the EMBL Data Library, February 1995
A; Rescription: Cloning of bovine CD40L and homology to bovine TNFA and TNFB. A; Reference number: S53090
A; Recession: S53090
                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: 248469; NID: 9732569; PIDN: CAA88363.1; PID: 9732570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 ILRLHE------NACLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 SGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN-- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 KKKEKNFE-----MHKGDQEPQIAAHV-----ISEASSKTTSVLQWAPKGYYTLSNNL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 MTLSNGK-LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN-- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 VTLENGKQLAVKRQGFYXIYTQVTFCSNRETLSQAP-----FIASLCLKSPSGSERI 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 PAPSAPAPAPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                           Length 261;
                                                                                                                                                                                                                                                                                                                                                                         11.1%; Score 185.5; DB 2; Length 25.1%; Pred. No. 3.3e-08; Live 50; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 25.1
nes 75; Conservative
                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-261 <MER>
                                                                                                                                                                                                                                              A; Status: preliminary
                                             CD40 ligand - bovine
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Matches
RESULT
S53090
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fas ligand - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C,Accession: A49266
R;Suda, T,; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tu A;Reference number: A49266; MUID:94084792

dihydrolipoamide S collagen alpha 1(I lymphotoxin alpha

95.5 94 93.5

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----SSLEKQIGHPSPPPE-----
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es 67; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : DNA
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                                                                                                                                                                                                                                                                                                                                                               Fas ligand - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type
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Best Local Si
Matches 67;
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A53062
A53062
Exa ligand - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #text_change 05-Nov-1999
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53062
R:Takahashi, T: Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; N.Cell 76, 969-976, 1994
A;Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in A; Reference number: A53062; MuID:94185175
A;Accession: A53062
A;Cross-references: GB:U06948; NID:9473564; PIDN:AAA17800.1; PID:9473565
                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LSHKVYM--RNFKYPGDLVLME-EKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 MKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AASIP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYL, 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------LEWEDTYGTALISGVKYKKGGLVINETGLYFVYSKVYFR-GQSCNNQPLNH- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 CRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----KKEPRSVAHLTGNPHSRSIP 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 GLGLGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PAASRSMFLALLGLG 57
               A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: B; Status: A;Molecule type: B;Molecule type: B;
                                                                                                                                                                                                                                                                                                                                                            ----PAASRSMFLALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIPSGSHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 DYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQV
                                                                                                                                                                                                                                                                                                     96;
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Best Local Similarity 22.7%; Pred. No. 7.1e-08;
Matches 72; Conservative 48; Mismatches 105; Indels
                                                                                                                                                                                                                                    Score 183; DB 2; Length 27; Pred. No. 5.9e-08; 42; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                         SSEEMGSG-----PGVPHEGPLHPAPSAPAPAP------
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SQLSLINFEESKTFFGLYKL 278
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                                                                                                                                                                                                                                    10.9%;
                                                                                                                                                                                                                                 Query Match 10.9
Best Local Similarity 23.4
Matches 75; Conservative
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A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
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A.T.L. Immunicator, v. 1577, 1574
A.T.L. Imman Fas 11gand: gene structure, chromosomal location and species specifici
A.R.Ference number: 138707; MUID:95127560
A.Accession: 138707
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A;Molecule type: mRNA
A;Residues: 1-281 cRES>
A;Cross-references: EMBL:U11821; NID:9595430; PID:9595431
A;Cross-references: EMBL:U11821; NID:9595430; PID:9595431
B;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, Biochem Biochem: Biochem: 204, 468-474, 1994
A;Tille: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350
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A;Cross-references: GB:D38122; DDBJ:D29820; NID:g601892; PID:d1007898; PID:g1369902
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C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Aug-1998
C;Accession: 138707; JC2340; S57565; I38554
R;Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
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                                         208 --KVYM--RNSKYPEDLVLME-EKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNISQL 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRM 118
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J. Exp. Med. 181, 71-77, 1995
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A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:9887455; PID:9887456
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A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:9624627; PID:9624628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 PGVPHEGPLHPAPSAPAPAPPAASR---------
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SLINFEESKTFFGLYKL 279
                                                                                                                                              SLLDPDQDATYFGAFKV 312
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C1701 Control of a mouse C1702 C1703 C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 KEETKKENSF--EMQKGDQNPQIAAHV-----ISEASSKTTSVLQWAEKGYYTMSNNLV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--M 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 -NLHEDFVFMKTIQRCNTGERSLSLL-----NCEEIKSQFEGFV-KDIM-----LN 101
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                                                                                                                                                    63;
                                                    Length 261;
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                                                                                                                                                    Indels
                                      9.4%; Score 157; DB 2; Lv 24.8%; Pred. No. 8e-06; tive 51; Mismatches 105;
                                                                                                                                               Conservative
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A; Accession: 153476
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-261 < RES>
A; Cross references: GB:L07414; NID:9180123; PIDN:AAA35662.1; PID:9180124
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A; Accession: S28017
A; Accession: S28017
A; Residues: 1-261 < HOL>
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R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.J.
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A;Reference number: JH0793; MUID:93094757
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R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
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A.Accession: $28852
A.Aoleoule type: mRNA
A.Residues: 1-261 <GAU>
A.Cross-references: EMBL:L07414; NID: 9180123; PIDN: AAA35662.1; PID: 9180124
A.Gross-references: EMBL:L07414; NID: 9180123; PIDN: AAA35662.1; PID: 9180124
A.Gross-references: EMBL:L07632; OMIM: 308230
A.Gross-references: GDB: 120632; OM
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Sate: 02-0ul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct-1999
C; Accession: I53476; S28017; JH0793; S26694; S28852; S25684; S30593
R; Gauchat, J.
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177 GSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQ 236
                                                                   ------LEWEDTYGIVLLSGVKYKKGGLVINETGLYFVYSKVYFRGQSCNN-----LP 206
                                                                                                                                                                                      LMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPS 296
                                                                                                                                                                                                                                                    207 LSHKVYMRNSKYPQDLVMME-GKMMSYCTTGQMWARSSYLGAVFNLTSADHLYVNVSELS 265
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A.Experimental source: peripheral blood T-cell
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A.Reference number: S26694; MUID:93076854
A.Status: preliminary
A.Nolecule type: mRNA
A.Residues: 1-261 GRA>
                                                                                                                                                                                                                                                                                                                                                                       LLDPDQDATYFGAFKV 312
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A; Molecule type: mRNA
A; Residues: 1-261 <SPR>
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A Accession: A27303

A; Molecule type: DNA

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A; Molecule type: DNA

A; Molecule type: DNA

A; Mossidues: 1-235 ASENA

A; Cross-references: GB:Y00467; NID:954830; PIDN:CAA68530.1; PID:954832

B; Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

B; Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

A; Title: Cloning and expression in Escherichia coli of the CDNA for murine tumor necr

A; Reference number: A25164; MUID:85298296
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R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashim Nucleic Acids Res. 13, 4417-4429, 1985
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R;Cseh, K.; Beutler, B.
T. Biol. Chem. 264, 16256-16260, 1989
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A; Residues: 1-230, "R. 232-235 cRES>
A; Residues: 1-230, "R. 232-235 cRES>
A; Cross-references: GB:M13049; NID:9202082; PIDN:AAA40457.1; PID:9202083
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A; Title: Characterization of high molecular weight glycosylated forms of murine tumor A; Reference number: A36696; MUID:91097531
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A; Residues: 70-87 c(SE)
A; Residues: 70-87 c(SE)
B; Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
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A;Titler, Identification of a common nucleotide sequence in the 3'-untranslated region
A;Reference number: 159058; MUID:86149365
A;Accession: IS9058
                                                                                                                                                                                                A; Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor A; Reference number: A93679; MUID:88067722
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C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage;
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
    A;Cross-references: GB:M38296; NID:q202086; PIDN:AAA40459.1; PID:q202087
A;Note: article in Russian with English abstract
R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 IVGPQRF----SGAP---AMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLS- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:20/Binding site: myristate (Lys) (covalent) #status predicted **84/Alanding site: carbohydrate (Ser) (covalent) #status predicted F:86/Binding site: carbohydrate (Sen) (covalent) #status predicted F:148-179/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 146.5; DB 1
25.6%; Pred. No. 5.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 25.69
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 62/3; 81/1; 97/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: A25164
A, Molecule type: mRNA
A, Residues: 1-235 <PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A36696
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Union intrioris datum at pine precursor.

C; Species: Equus cachectin; TNF alpha
C; Species: Equus caballus (domestic horse)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C; Accession: J01344
R; Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A; Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A; Reference number: J01344; MUID:92084125
A; Molecule type: DNA
A; Residues: 1-234 A:SUX>
A; Cross-references: GB:M64087; NID:9164244; PIDN:AAA30959.1; PID:9164245
C; Comment: This protein is an important proximal mediator of endotoxemia.
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: tumor necrosis factor
C; Superfamily: tumor necrosis factor alpha #status predicted <TUN>
F; 19-20/Binding site: myristate (Lys) (covalent) #status predicted
F; 146-178/Disulfide bonds: #status predicted
F; 146-178/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nilernate names: cachectin; TNF alpha
C; Species: Mus musculus (house mouse)
C; Species: Musculus (house mouse)
C; Species: Subject (house)
C; Specie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.9%; Score 149; DB 1; L. 24.1%; Pred. No. 3.2e-05; Live 38; Mismatches 72;
                                                                                                                                                                                                                                           tumor necrosis factor alpha precursor - horse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor alpha precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 PSLLD-PDQDATYFG 308
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258 LKL 260
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A; Residues: preliminary
A; Residues: 1-234 < AMS.)
A; Cross-references: EMBL.X56756; NID:9297806; PIDN:CRA40076.1; PID:9297807
B; Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A; Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A; Reference number: S13114; MUID:91067496
A; Reference number: S13114
A; Residues: 1-62, 64-234 < YOU>
C; Reywords: alternative splicing: cytokine; cytotoxin; glycoprotein; lym F; 1-77, Domain: propeptide #status predicted < PRO>
C; Keywords: alternative splicing: cytokine; cytotoxin; glycoprotein; lym F; 1-77, Domain: propeptide #status predicted < PRO>
F; 20/Flainding site: carbohydrate (Ser) (covalent) #status predicted
F; 82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 146-178/Disulfide bonds: #status predicted
F; 146-178/Disulfide bonds: #status predicted
A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A:Reference number: S48118; MUID:92155784
A:Accession: S48118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumor necrosis factor alpha precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C;Accession: S11688
R;McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A;Title: Gene sequence of feline tumor necrosis factor alpha.
A;Reference number: S11688; MUID:91016860
A;Accession: S11688; MUID:91016860
A;Accession: S11688; MUID:91016860
A;Accession: S11688
A;Accession: S11688
A;Cocssion: S11688

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C:Superfamily: tumor necrosis factor
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19, 20/Binding site: myristate (Lys) (covalent) #status predicted
F:91/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 IVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSG----SHKVTLSSWYH 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 QLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYSQVLFRGHGCPSTPLFLTHTISRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.4%; Score 141; DB 1; Length 234; 25.8%; Pred. No. 0.00015; tive 31; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 DRGWA-KISNMTLSNG-KLRVNQ-----DGFYYLYANICFRHH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Conservative
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Best Local Similarity
Matches 51; Conserv
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Nalternate names: cachectin; TNF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: JH0529; S48118; S13114; S20661
R;Green 109, 203-210, 1991
A;Reference number: JH0529; MUID:92112044
A;Residues: 1-334 <GRE>
A;Cross_references: EMBL.X55152; NID:91405; PIDN:CAA38952.1; PID:91406
A;Experimental source: alveolar macrophage
A;Experimental source: alveolar macrophage
E;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic DNA
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R; Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A; Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic A; Reference number: $22052
A; Reference number: $22052
A; Reference number: $22052
A; Accession: $22052
A; Accession: $22052
A; Accession: $22052
A; Residues: 1-233 <SAN>
A; Residues: 1-233 <SAN>
A; Residues: 1-233 <SAN>
A; Cosson references: EMBL: X62141; NID:938159; PIDN: CAA44068.1; PID:938160
C; Genetics:
A; Introns: 62/3; 78/1; 94/1
C; Superfamily: tumor necrosis factor
C; Reywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F; 19,20/Binding site: myristate (19x) (covalent) #status predicted
F; 81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F; 145-177/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S22052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                             160 RFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW-----YEPIYLGGVFQLEKGDQLSA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL-----M 238
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                                   ----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
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ilarity 25.6%; Pred. No. 9.3e-05;
Conservative 36; Mismatches 70;
                                                                                                                                                                                                            QVSNPSLLD-PDQDATYFG 308
                                                                                                                                                                                                                                                                                       213 EVNLPKYLDFAESGOVYFG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLLD-PDQDATYFG 308
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Best Local Similarity
Matches 50; Conserv
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C; Complex: homotrimer
                                                               A; Molecule type: DNA
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             A; Accession:
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Concerns and an application TREP
Concerns and an application TREP
Concerns and an application TREP
Concerns and Co
                                10;
                                                                                                                                                                                       158 RFAVSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YEPIYLGGVFQLEKGDRLST 210
                              Gaps
                                                                                     GAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTL 183
                                                                                                                                      GPQREELPH--GLQLINPLPQTLRSS-----SRTPSDKPVAHVVAN----PEAEGQLQR 104
                                                                                                                                                                                                                                                                                                     ---MYYVVK----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISI
                                40;
                                74; Indels
     0.00018;
                                Mismatches
  25.1%; Pred. No.
                                35;
                                                                                                                                                                                                                                                                                                                                                                                                                                      211 EINLPAYLDFAESGOVYFG 229
                                                                                                                                                                                                                                                                                                                                                                                                          OVSNPSLLD-PDODATYFG
                                Conservative
Best Local Similarity
Matches 50; Conserv
                                                                                                                                      22
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R.D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter re
A;Reference number: 154522: MUID:94102809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          out detriment to normal cells. It can also act synergistically with interferon gamma C; Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos ut are produced by different cell types and have different induction kinetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Residues: 1-8 < DAL>
A/Cross-references: 1-8 < DAL>
A/Cross-reference number: A59183, MUD: 93018820
A/Crotents: annotation; identification of myristylated lysines
A/Crotents: annotation; identification of myristylated lysines
A/Crotents: A6918-2354, 1985
A/Title: Human tumor necrosis factor Production, purification, and characterization.
A/Reference number: A92311; MUD: 95130974
A/Crotents: annotation; disulfide bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;19,20/Binding site: myristate (Lys) (covalent) #status experimental F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental F;145-177/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                              natural human tumor-necrosis factor-alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 QTKVNLLSAIKSPCQRETPEGAEAKPW----YEPIYLGGVFQLEKGDRLSAEINRPD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 IVGPQRFSGAPAMMEGSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSSWYHD 189
                                                                                                                              A;Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
A;Experimental source: U-937 cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 VVK----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 RGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL-----MVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 233;
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                                                                                                                                                                                                           R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3 -6p21.3
A;Introns: 62/3; 78/1; 94/1
                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S62610; MUID: 96202967
A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || : |||
217 YLDFAESGOVYFG 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 77-99 <TAK>
                                                                                     -233 <MAR>
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C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: 146047; S24642
C;Accession: 146047; S24642
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and A;Reference number: 146046; MUID:94083525
A;Accession: 146047
                                                                                                                                                                                                                                                               factor/cachectin (TNF) gene from Peromyscus
tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Aate: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C;Aacession: 154490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromys A;Reference number: 154490; MUID:92218012
A;Accession: 154490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cross references: GB:M59233; NID:9202506; PIDN:AAA40596.1; PID:9202507
C;Genetics:
A;Gene: PITNF
A;Introns: 62/3: 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Genetics: Gy:Superfamily: tumor necrosis factor
C;Reywords: 91ycoprotein: lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVGPQRFSGAP-----AMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSS 185
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 233;
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Similarity 25.8%; Pred. No. 0.00064;
51; Conservative 30; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 135.5; DB 2 Pred. No. 0.00044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary; translated from GB/EMBL/DDBJ
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C; Superfamily: tumor necrosis factor
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Best Local Similarity
Matches 51; Conserva
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                                                                      Vuncor inecrosis at accord alpha precursor - rabbit Cisper-1999 inecrosis at accordenction. The alpha of Space Salvanor and Sep-1999 inecession: As2454; As2451, As2645. Solvanor Conference concession: As2454; As2451, Solvanor Cisper-1999 inext_change 04-Feb-2000 Cisper-1999 inequal Cis
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22.6%; Pred. No. 0.0003;
ative 31; Mismatches 99;
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INTERPRO; IPR00254; TNF; 1.
PRAM; PF00225; TNF; 1.
PROSITE; PS0025; TNF_1: 1.
PROSITE; PS0049; TNF_2: 1.
Cytokine; Transmembrane; Signal-anchor; Apoptosis.

Cytokine; Transmembrane; Signal-anchor; Apoptosis.

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
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Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
Wicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
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"Identification and characterization of a new member of the TNF
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Immunity 3:673-682(1995).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN) (APO-2 LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Induction of apoptosis by Apo-2 ligand, a new member of the tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A., Ashkenazi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                             281 AA
                                                                                                                                                                                               ALIGNMENTS
RRPO_PMV
60IM_PSEPU
MAPA_RAT
NKR9_HUMAN
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U37518; AAC50332.1; -. EMBL; U57059; AAB01233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFSF10 OR TRAIL OR APO2L.
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=PLACENTA;
MEDLINE; 96278649.
                                                                                                                                                                                                                                                                                                                                                             TRAI_HUMAN P50591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (APO-2L)
                                                                                                                                                                                                                                                                                          TRAI_HUMAN
                                                                                                                                                                                                                                                                                                                                                                HID DOOR WAY A WAY
```

marmota mon rattus norv

sus scrofa

P23563

mus musculu cervus elap homo sapien capra hircu macropus eu saccharomyc mus musculu saccharomyc

035734 P16599 P41155 P51743

NFC_MOUSE

FNFA_RAT

NFC_HUMAN 'NFA_CAPHI NFA_MACEU

206643

003703 064467 P36135

YMD7_YEAST G3PT_MOUSE

TK22_YEAST

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EMBL; Z48469; CAA88363.1; -.
  DOMAIN
CARBOHYD
                          SEQUENCE
                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                            289 LI
                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
TNF5_BOVIN
                                                                                        Matches
                                                                                                                                                                                         64
                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FT
                                                                                                                                       qq
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                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                   PAASRSMFLALLGLGLGGOVVCSIALFLYFRAQMD--PNRISEDSTHCFYRILRLHENAGL 100
                                                                                                                                                   QDSTLESEDTLPDSCRRMKQAFQGAVQK------ELQHIVGPQRFSGAPAMM 146
                                                                                                                                                                                                     196
                                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                      256
                                                                                                                                                                                                                                                                              224
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE; 96111955.
Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
Goodwin R.G.;
                                                                                                                  WDP--NDEESMNSPCWQVKWQLRQLVRKMILRTSEETISTVOEKQQNISPL-----
                                                                                                                                                                                                     EGSWLDVAQRGKPEAQPFAHLT - - - - INAASIPSGSHKVTL - - - - SSWYHDR-GWAKIS
                                                                                                                                                                                                                           -----VRERGPORVA--AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS
                                                                                                                                                                                                                                                     NMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK
                                                                                                                                                                                                                                                                  Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                      GGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                   SARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification and characterization of a new member of the TNF family that induces apoptosis.";
Immunity 3:673-682(1995).
                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!-| FUNCTION: INDUCES APOPTOSIS.
-!-| SUBUNIT: HOMOTRIMER (POTENTIAL).
-!-| SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
-!-| TISSUE SPECIFICITY: WIDESPREAD.
-!-| SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                  Length 281;
                                                                           Indels
EXTRACELLULAR (POTENTIAL).
DDAAAF78DAAB2F6D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TMF-RELATED APOPTOSIS INDUCING LIGAND (FRAIL PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal-anchor; Apoptosis
                                                                          54; Mismatches 113;
                                                  DB 1;
                                                 15.4%; Score 258.5; DB 1 26.4%; Pred. No. 2.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                            291 AA
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
281 E. 32509 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U37522; AAC52345.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1. Cytokine; Transmembrane; Si
                                           Ouery Match
Best Local Similarity 26.4%
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:107414; TRAIL.
INTERPRO; IPR000478; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus (Mouse)
39
281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 96111955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNFSF10 OR TRAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                            TRAI_MOUSE
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                          P50592;
                                                                                                                                                                                                                                                                                                                                                                RESULT 2
TRAI_MOUSE
                                                                                                                                                                                                  147
                                                                                                                        10-
                                                                                                                                                   101
                                                                                                                                                                            65
                                                                                                                                                                                                                             114
                                                                                                                                                                                                                                                   197
                                                                                                                                                                                                                                                                              166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus
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                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mertens B.E.L.C., Muriuki M., Gaidulis L.; "Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 NMTLSNGKLRVNQDGFYYLYANICFRHHE---TSGSVPTDYL---QLMVYVVKTSIKIPS 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 SHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAF 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 PIVLMKSARNSCWSRDAEYGLYSIYQGGLFELKKNDRIFVSVTNEHLMDLDQEASFFGAF 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---TDEDFWDST--DGEILNRPCLQVKROLYQLIEEVTLRTFQDTISTVPEKQLSTPPLP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 RG-----GRPQ-KVAAHITGITRRSNSALIPISKDGKTLGOKIESWESSRKGHSFLN 169
                                                                                                                                                                                                                                                                                                                                                                                                                        93 RLHENAGLODSTLESEDTLPDSC----RRMKQAFQGAVQKELQHIVG--PQRFSGAPAMM 146
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGSWLDVAQRGKPEAQPFAHLT----INAASIPSGSHKVTL----SSWYHDR-GWAKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ALLGLGLGQ-----VVCSIAL------FLYFRAQMD--PNRISEDSTHCFYRIL
                                                                                                                                                                                                                                                                                                                                                         6 ALKDLSFSQHFRMMVICIVLLQVLLQAVSVAVTYMYFTNEMKQLQDNYSKIGLACFSK--
                                    N-LINKED (GLCNAC. . .) (POTENTIAL). 3FEACAB9F0D7D802 CRC64;
                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                  Length 291;
                                                                                                                                                                                                                              50; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T
      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                  Score 244; DB 1;
Pred. No. 4.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          261 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and tumor necrosis factor alpha.";
Immunogenetics 42:430-431(1995).
                                                                     MW;
                                                                                                                                                               14.68; 27.58;
291
52
33477 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNFSF5 OR CD40LG OR CD40L.
                                                                                                                                                                                                                                  83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=BLOOD;
MEDLINE; 96006582.
                                                                  291 AA;
                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996
01-OCT-1996
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 KV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNF5_BOVIN
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DOMAIN
                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
FASL_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                      q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECTION 194084792.

Suda T., Takahashi T., Golstein P., Nagata S.;
Sell 75:1169-1178(1993).
-!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTORIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOWIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES, KIDNEY AND LUNG.
                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                             91 ILRLHE------NAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRF 139
                                                                                                                                                                                                                                                                                                             --NLHEDFVFMKTIQRCNKGEGSLSLL-----NCEEIRSRFEDLVKDIMQN----KEV 104
                                                                                                                                                                                                                                                                                                                                                                       105 KKKEKNPE-----MHKGDQEPQIAAHV-----ISEASSKITSVLQWAPKGYYILSNNL 152
                                                                                                                                                                                                                                                                                                                                              140 SGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN-- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mětazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN. MAY BE RELEASED
BY CLEAVAGE FORM THE CELL
                                                                                                                                                                                                                                         32 PAPSAPAPAPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 LMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MILSNGK-LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--
                                                                                                                                                                                                                                                                                                                                                                                                                         153 VTLENGKQLAVKRQGFYYIYTQVTFCSNRETLSQAP-----FIASLCLKSPSGSERI
                                                                                                                                                                                                                                                                  PSPRSVATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDER----
                                                                                                                                                                                                                   63;
                                                                                                                                                                                        Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2
                                                                                                                                                                                                                  50; Mismatches 111; Indels
                                                                                                   (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                              ycoprotein; Signal-anchor.
                                                                                                                                        N-LINKED (GLCNAC, ...) (
8491FEFB30A787FD CRC64
                                                                                                                                                                                          DB 1;
                                                                                                                                                                                          Score 185.5; DB 1
Pred. No. 2.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T CELLS, OR BOTH.
SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II MEMBRANE
INTO THE EXTRACELLULAR FLUID, PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                             261 EX
218 PC
240 N.
29242 MW;
                                                                                                                                                                                          11.1%;
25.1%;
         INTERPRO, IPRO00478; -. PFAM, PF0229; TNF; 1. PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1. Cytokine; Transmembrane; Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFSF6 OR APT1LG1 OR FASL. Rattus norvegicus (Rat).
                                                                                                                                                                                                                75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                       46
                                                                                                             47
178
240
261 AA;
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAS ANTIGEN LIGAND.
HSSP; P29965; 1ALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                              DOMAIN
DISULFID
CARBOHYD
SEQUENCE
                                                                                     TRANSMEM
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                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal-anchor; Apoptosis.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 CRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 --LSHKVYM--RNFKYPGDLVLME-EKKLNYCTTGQIWAHSSYLGAVFNLTVADHLYVNI 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 SSEEMGSG-----PGVPHEGPLHPAPSAPAPAPPP-------PAASRSMFLALL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
2899BIBAB6ACEAC6 CRC64;
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 183; DB 1; Length 278; 23.4%; Pred. No. 4.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FASL_MOUSE STANDARD; PRT; 279 AA. P41047; 061217; 01-FEB-1995 (Rel. 31, Created) 1-FEB-1995 (Rel. 31, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-PRO.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNFSF6 OR APTILG1 OR FASL OR GLD.
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SQLSLINFEESKTFFGLYKL 278
                                                                                                                                                                                                                                                               INTERPRO; IPR000478; --
PFAM; PF00229; TNF; 1
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Transmembrane; Glyc
                                                                                                                                                                                                                                           EMBL; U03470; AAC52129.1; -.
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278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
247
257
278 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
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100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                           LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOWAL RECESSIVE DISEASE RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
                                                                                        Peitsch M.J., Tschopp J.J.; "Comparative molecular modelling of the Fas-ligand and other members
        "Geheralized lymphoproliferative disease in mice, caused by a point mutation in the Fas ligand.";
                                                                                                                                                                                                   Ø
                                                                                                                                                                                                                                                                   Fenner M.H., Shioda T., Isselbacher K.J.;
"Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
                                                                                                                                                                         Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E., rough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.; "The mouse Fas-ligand gene is mutated in gld mice and is part of TWF! family gene cluster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Signal-anchor; Apoptosis;
                                                                                                                                                                                                                                                                                                                                                   Hahne M., Peitsch M.C., Irmler M., Schroeter M., Lowin B.,
                                                                                                                                                                                                                                                                                                       Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                       FROM N.A., AND 3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRO-RICH
                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION OF VARIANT GLD.
                                                                                                                         Mol. Immunol. 32:761-772(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U06948; AAA17800.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U10984; AAA19778.1; -. S76752; AAB33780.1; -. U58995; AAB02915.1; -. P01375; 2TUN.
                     Fas ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROŠITE; PS00251; TNF_1; 1.
PROŠITE; PS50049; TNF_2; 1.
Cytokine; Transmembrane; Gly
                                                                                                                                                                                                                        [mmunity 1:131-136(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
100
279
69
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INTERPRO; IPRO00478; -
PFAM; PF00229; INF; 1.
                                Cell 76:969-976(1994)
T., Nagata S.;
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                         MEDLINE; 96091792.
                                                                                                                                                              95196085.
                                                                              MEDLINE; 95388076
                                                                                                                the TNF family
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101
4
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                                                      SEQUENCE FROM I
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                                                                                                                                                                                                                                                                                            two amino
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TRANSMEM
                                                                                                                                                              MEDLINE;
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HSSP;
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13;
                                 N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
T -> A (IN STRAIN BALB/C).
E -> G (IN STRAIN BALB/C).
F -> L (IN GLD; ABOLISH BIDING OF FASL TO ITS RECEPTOR).
MW; 37972E2728E0A1CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 --KVYM--RNSKYPEDLVLME-EKRLNYCTTGQIWAHSSYLGAVFNLTSADHLYVNISQL 262
                                                                                                                                                                                                                                                                                                                                                                                                   58 LGQVVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 MKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTIN--AASIP 175
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                              --PAASRSMFLALLGLG 57
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Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
"Human Fas ligand: gene structure, chromosomal location and species specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                             236 QLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Fas ligand mediates activation-induced cell death in human T
                                                                                                                                                                                                                                                     Length 279;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Schaetzlein C.E., Poehlmann R., Philippsen P., Eibel H.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
TNFSF6 OR APTILGI OR FASL.
                                                                                                                                                                                                                                                                                       48; Mismatches 105;
                                                                                                                                                                                                                                                  10.9%; Score 182; DB 1; 22.7%; Pred. No. 5.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                 BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                            13 RSSEEMGSGPGVPHEGPLHPAPSAPAPAP----
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                                                                                                                                                                                          31442 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 SLLDPDQDATYFGAFKV 312
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SLINFEESKTFFGLYKL 279
                                                                                                                                                                                                                                                                                       Conservative
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 51
231
117
1182
248
258
258
258
2184
218
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                                                                                                                                                                                          279 AA;
                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 95105731.
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45
200
117
1182
248
258
258
1184
218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lymphocytes.
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                                                       CARBOHYD
CARBOHYD
                 DISULFID
                                                                                              CARBOHYD
                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                   Query Match
                                     CARBOHYD
                                                                                                                VARIANT
                                                                                                                                                     VARIANT
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FASL_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135
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297 LLDPDQDATYFGAFKV 312
                                                                                                                                                                     |:: :: |:|| :|:
266 LVNFEESQTFFGLYKL 281
                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                            TNF5_HUMAN
                                                                                                                                                                                                                                                          P29965
                                                                                                                                                                                                                    RESULT 7
TNF5_HUMAN
                          125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                         MALSUMULE M., Nakanishi Y., Obba Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOXING T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T CELLS, OR BOTH.
-!- SUBUNIT: HOMOTRIMER (PROBABLE).
-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
EXTRACELLULAR (POTENTIAL)
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POLY-PRO.
BY SHMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
CYtokine; Transmembrane; Glycoprotein; Signal anchor; Apoptosis.
                       Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara Fusamoto H., Kamada T.; Role of Fas ligand in apoptosis induced by hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 281;
                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                          Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                         Biochem. Biophys. Res. Commun. 204:468-474(1994).
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                                                                                                                                                   SEQUENCE OF 1-10 FROM N.A.
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Best Local Similarity 21.2%
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO; IPR000478; -.
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281 AA;
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SEQUENCE FROM N.A. MEDLINE; 95071350.
                                                                                                                                                                  TISSUE=BLOOD;
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MIM; 134638;
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                                                                                                                                                          ----SSLEKQIGHPSPPPE-------KKELRKVAHLTGKSNSRSMP- 159
119 KQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLT--INAASIPS 176
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01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CD40 LIGAND (CD40-L) (TNF-ELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN GP39) (CD154 ANTIGEN).
TNFSF5 OR CD40LG OR CD40L OR TRAP.
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Macduff B.M., Sato T.A., Maliszewski C.R., Fanslow W.C.;
"Recombinant human CD40 ligand stimulates B cell proliferation and
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Gauchat J.F.M., Aubry J., Mazzei G.J., Life P., Jomotte T., Elson
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Braesch-Andersen S., Noelle R.J., Stamenkovic I., Ledbetter J.A.,
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                                                                                                                                                                              MEDFINE; 96131874.
Karpsusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
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                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97295077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kroczek R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
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                                                                                                                                                                                                                                                                                                                                 ligand."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                      Matsuda
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                                                                                      DISEASE: DEFECTS IN CD40LG ARE THE CAUSE OF AN X-LINKED IMMUNODEFICIENCY WITH HYPER-IGM (HIGMI), AN IMMUNOGLOBULIN ISOTYPE SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE) RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
             SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                            PNEUMOCYSTIS CARINII PNEUMONIA AND INFRACTABLE DIARRHEA DUE TO CARPTOSPORIDIUM INRECTION. DESPITE SUBSTITUTION TREATMENT WITH INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR, WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
DATABASE: NAME-COJ01DASSE;
NOTE-EUROPEAN COJ01D DEFECT DATABASE (MUTATION DB);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
Discase mutation; Polymorphism.
CytopLasMIC (POTENTIAL).
                                                         -!- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                  WWW="HTTP://WWW.EXPASY.CH/CD40LBASE,";
FTP="FTP://FTP:EXPASY.CH/DATABASES/CD40LBASE";
DATABASE: NAME=FROW; NOTE=CD quide CD154 entry;
WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD154.HTM".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=vAR_007515.
SE -> RG (IN H1GM1).
/FTId=vAR_007516.
W -> C (IN H1GM1).
                                                                              1-LIMPROCLIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M -> R (IN H1GM1).
IN IMMUNOGLOBULIN CLASS SWITCHING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VAR_007514.
V -> A (IN H1GM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /FTId=VAR_007513.
A -> E (IN H1GM1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTIG=VAR_007517.
W -> G (IN H1GM1)
/FTIG=VAR_007518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D31797; BAA06599.1; -
D31793; BAA06599.1; -
D31794; BAA06599.1; JOINED.
D31795; BAA06599.1; JOINED.
D31796; BAA06599.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X68550; CAA48554.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 215017; CAA78737.1; -. EMBL; X67878; CAA48077.1; -. EMBL; L07414; AAA35662.1; -.
                                            EXTRACELLULAR SOLUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR000478; -. PFAM; PF00229; TNF; 1.
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218
240
36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . $25684; $25684.

. $26694; $26694.

. $28017; $28017.

. $28852; $28852.

. JH0793; JH0793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1ALY; 17-SEP-97
                                                                        T-LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
178
240
36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 308230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
PIR;
PIR;
PIR;
PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB;
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W -> R (IN HIGMI)

140

140

VARIANT

X-linked hyper-igm syndrome.";
Hum. Genet. 99:624-627(1997).
-i--FUNCTION: MEDIATES BASENCE OF CO-STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.

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[3]
3D-STRUCTURE MODELING OF 115-260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNFSF5 OR CD40LG OR
                                                                                                                                                                                                                                                   234 AA;
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 92244364.
                                                                                                                                                                                                                      36
147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF5_MOUSE
P27548;
                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 54
                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                             PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
TNF5_MOUSE
                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GP39)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283
                                                                                                                                                                                                                                                                                                                                                                                                       176
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염
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                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am. J. Physiol. 273:L524-L530(1997).

-!- FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF EUNCTTONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEURIN I SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CRETAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMOTRIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELULAR SOLUBLE FORM (BY SIMILARITY).
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING (BY SIMILARITY).
DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
                                                                                                                                                                                                                                                    LRLHE-----NAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFS 140
                                                                                                                                                                            GAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--M 198
                                                                                                                                                                                                      102 KEETKKENSF--EMQKGDQNPQIAAHV----ISEASSKTTSVLQWAEKGYYTMSNNLV 153
                                                                                                                                                                                                                                   TLSNGK-LRVNQDGFYYLYANICF-RHHETSGSVPIDYLQLMVYVVKTSIKIPSSHN--L 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
"Airway inflammation induced by recombinant guinea pig tumor necrosis
                                         Gaps
                                                                33 APSAPAPAPAPASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCFYRI 91
                                                                                                                                                                                                                                                                                        MKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                        :| : | | | :| :| :| :| SPRSAATGLP--ISMKIFMYLLTVFLITQMIGSALFAVYLHRRLD--KIEDER-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                        63;
            Length 261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAINH-HARPLEX; TISSUE-LUNG;
Yuan H.T., Kelly F.J., Bingle C.D.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
          10.2%; Score 171.5; DB 1; 25.2%; Pred. No. 3.5e-07; ive 49; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                         234 AA
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                        Best_Local Similarity 25.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-DUNKIN-HARTLEY;
MEDLINE; 97462215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND MALNUTRITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor-alpha.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNF OR TNFA
                                                                                                                                                                                                                                                                                                                                                                                         CAVPO
           Query Match
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TNFA_CAVPO
                                                                                                                                                                            141
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|||| || || : | :
55 VIGPQREEQFSSGPPF------RPLAQTLTLRSASQNDNDKPVAHVVANQQAEE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PFAHLTINAASIP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 LLLTHTVSRLAVSYPEKVNLLSAIKSPCOKETPEGAERKPW-----YEPIYLGGVFQL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ġ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-ANY-2000 (Rel. 39, Last annotation update)
CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSHKVTLSSWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 E-----LQWLSKRANALLANGMGLSDNQLVVPSDGLYLIYSQVLFK-----GQGCPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQLMVYVVKTSIKIPSSHNLM------KGGSTKNWSGNSEFHFYSINVGGFFKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Armitage R., Fanslow W., Sato T.A., Clifford K.N., Strockbine L., Macduff B.M., Anderson D.M., Gimpel S.D., Davis-Smith T., Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spriggs M.K.; "Molecular and biological characterization of a murine ligand for
                                                                                                                             HSSP, P01375; TTU.
HSSP, P01375; TTU.
HNTERPRO; IPR000478; -
INTERPRO; IPR002959; -
PRINTS; PR01234; TNE. II.
PRINTS; PR01234; TNEALPHA.
PROSITE; PS00251; TNFIL; 1.
PROSITE; PS0049; TNFIL; 1.
CYLCKING; CYLCKOXIN; TRANSMembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7272C940393E7E9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 IVGPQR---FSGAPAMMEGSWLDVAQRGKPEAQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%; Score 157; DB 1;
26.1%; Pred. No. 4.7e-06;
tive 26; Mismatches 65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ¥
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25793 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMILARITY TO THE TNF FAMILY.
MEDLINE; 92310561.
Farrah T., Smith C.A.;
"Emerging cytokine family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD40L.
                                                                               EMBL; U39839; AAB06492.1;
                                                                                                         EMBL; U77036; AAB19210.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         56
178
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                                                                                                                                                                                                                                                                                                                                                                                                                  234
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295 PSLLD-PDQDATYFG 308
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                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                       SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
         Peitsch M.C., Jongeneel C.V.;
"A 3-D model for the CD40 ligand predicts that it is a compact trimer
similar to the tumor necrosis factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VNLHEDFVFIKKLKRCNKGEGSLSLL-----NCEEMRROFEDLVKDITLNKE---- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------EKKENSF--EMQRGDEDPQIAAHVVSEA-----NSNAASVLQWAKKGYYTM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SERILLKAANTHSSSQLCEQQ--SVHLGGVFELQAGASVFVNVTEASQVIHRVGFSSFGL 257
                                                                                                                                                                                                                                                                                                                                                                      CTTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILRLHE------KELQHIV 134
                                                                                                                                                                                                                                                                                                                                                           Glycoprotein; Signal-anchor; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPSAPAPAPAPASRSMFLALLGLGL-GQVVCSIALFLYFRAQMDPNRISEDSTHCFYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISNMT-LSNGK-LRVNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIK--IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGA
                                                                                                               EXTRACELLULAR SOLUBLE FORM.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
                                                                                                                                                                                                                                                                                                                                                                                                                            LINKED (GLCNAC. . .) (POTENTIAL). 7E0F34F7473668B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72;
                                          INT. IMMUNO1. 5:233-238(1993).
-!-|FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF C
STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSPRSVATGLP--ASMKIFMYLLTVFLITQMIGSVLFAVYLHRRLD--KVEEE----
                                                                                                                                                 SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.4%; Score 157; DB 1; Length 26
24.8%; Pred. No. 5.4e-06;
ive 51; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         29396 MW;
                                                                                                                                                                                                                                                                  EMBĹ; X65453; CAA46448.1; -.
                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Transmembrane; Gl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 24.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      260
217
239
                                                                                                                                                                                                                                                                                                 MGD; MGI:88337; TNFSF5.
                                                                                                                                                                                                                                                                                                             NTERPRO; IPR000478; -.
                                                                                                                                                                                                                                                                                        1CDA; 31-0CT-93
                                                                                                                                                                                                                                                                              $21738
                                                                                                                                                                                                                                                                                                                                                                                                      47
177
239
260 AA;
                                                                                                                                                                                                                                                                                                                        PFAM; PF00229; TNF;
93200072
                                                                                                                                       T-LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                  23
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TNFA_HORSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
E79ACE91143DF373 CRC64;
                                                                                                                                                                                                                                                                                                                                            Su X., Morris D.D., McGraw R.A.;
"Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor alpha.";
Gene 107:319-321(1991).
-!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN I SECRETION, IT CAN STIMULATE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SÜBÜNIT: HOMOFRIMER.
-:- SÜBÜNIT: HOMOFRIMER.
-:- SÜBÜLÜLAR LÖCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLÜLAR SÖLÜBLE FORM.
-:- PTM: THE SÖLÜBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
-:- SIMILARITY: BELONGS TO THE TÜMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 SYPSKVNLLSAIKSPCHTESPEQABAKPW-----YEPIYLGGVFQLEKGDQLSABINQ 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 IVGPQRFSGAPAMMEGSWLDVAQRGK-----PEAQPFAHLTINAASIPSGSHKVTLSSWY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                    Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01234; TNECROSISFCT.
PRINTS; PR01235; TNFALPHA.
PROSITE; PS050451; TNF_2; 1.
PROSITE; PS55049; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
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24.1%; Pred. No. 2.2e-05;
ive 38; Mismatches 72; Indels
                             01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR PRECURSOR (INF-ALPHA) (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
TUMOR NECROSIS FACTOR.
      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M64087; AAA30959.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPR000478; -. INTERPRO; IPR002959; -.
                                                                                                                                                    Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00229; TNF; 1.
01-APR-1993 (Rel. 25, 01-APR-1993 (Rel. 25, 15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JQ1344; JQ1344.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01375; 1TNF
                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
MEDLINE; 92084125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
36
146
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                                                                                                                             INF OR TNFA
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DISULFID
SEQUENCE
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AND MALNUTRITION.
                                                                                                                                                                                                          295 PSLLD-PDQDATYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 96003435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNF OR TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                     TNFA_MACMU P48094;
                                                                                                                                                                                                                                                                                                                                                                                         TNFA_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A PACTOR OF THE 
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 VIGPOREEFPKDPSLI--SPLAQAVRSSSRTPSDKPVAHVVAN----PQAEGQL---QWL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL-----M 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 IVGPQR--FSGAPAMMEGSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSSWY 187
                                                                                                                                                                                                                                                                                                                                                                                Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertcbrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO, IPR002959; -.
INTERPRO, IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTECLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6ABF2C3AB132C217 CRC64;
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25.6%; Pred. No. 2.4e-05;
Live 38; Mismatches 68;
                                                                                                                                                                              233 AA
                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB000513; BAA19131.1; -. HSSP; P01375; 1TNF.
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Best Local Similarity 25.6°
Matches 50; Conservative
1: || : || | 110
216 PNYLDFAESGQVYFG 230
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000478; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=LYMPHOCYTES;
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                                                                                                                                                                                                                                                                                                                                                          TNF OR TNFA.
                                                                                                                                                                              INFA_MACFA
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INTERPRO, IPRO0255...

R PRAM, PRO0259, TUE: 1.

R PRINTS; PR01234; TNECROSISECT.

DR PRINTS; PR01235; TNFALPHA.

DR PROSITE; PS00251; TNF_1: 1.

DR PROSITE; PS50049; TNF_2: 1.

KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.

TY 233 TUMOR NECROSIS FACTOR.

ORFF85050595FD59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNIOT. THE TABLE SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN THOM CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INVERLEDRIN I SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
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239 VYVVK----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSN 294
                                                                                                                                                                               162 SYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YEPIYLGGVFQLEKGDRLSAEINL 214
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BY GENERAL ILL HEALTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.; "Comparative sequence analysis of cytokine genes from human and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF CANCER AND INFECTION, AND IS CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 155:3946-3954(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
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                                                                                                                                                                                                                                                                                                     1 | | : | | | 215 PDYLDFAESGQVYFG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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£2888£££2888££2888££28888££28888££2888££2888££2888££28886££288886868888868688888868888888
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"Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression.";
                                                        187
                                                                     ::|||| | |::: | | | |:
55 VIGPQREEFPRDPSLI--SPLAQAVRSSSRTPSDKPVAHVVAN----PQAEGQL---OWL 105
                                                                                                                    106 NRRANALLANGVELTDNQLVVPSEGLYLIYSQVLFK----GQGCPSNHVLLTHTISRIAV 161
                                                                                                                                                                 162 SYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YEPIYLGGVFQLEKGDRLSAEINL 214
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and expression in Escherichia coli of the cDNA for murine
                                                       133 IVGPQR--FSGAPAMMEGSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSSWY
                                                                                                     HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL-----M
                                                                                                                                                  239 VYVVK----TSIKIPSSHNLMKGGSTKNWSGNSFFHFYSINVGGFFKLRAGEEISIQVSN
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.; "Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3'-untranslated region of mRNA molecules specifying inflammatory mediators.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shakhov A.N., Nedospasov S.A.; "Molecular cloning of genes coding for tumor necrosis factor. Complete nucleotide sequence of the genome copy of TNF-alpha in
                                 39;
         Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 86149365.
Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pennica D., Hayflick J.S., Bringman T.S., Palladino M.A.,
Goeddel D.V.;
                                 Indels
                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identification of a common nucleotide sequence in the
                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         necrosis factor.";
Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986)
         Score 147.5; DB Pred. No. 2.9e-05;
                                                                                                                                                                                                                                                                                 235 AA.
                               38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 13:4417-4429(1985)
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                          P06804; 062326;
01-JAN-1988 (Rel. 06, Created)
01-MAR-1989 (Rel. 10, Last seq
30-MAY-2000 (Rel. 39, Last ann
        8.8%;
                                 50; Conservative
                                                                                                                                                                                                 295 PSLLD-PDQDATYFG 308
                                                                                                                                                                                                                       215 PDYLDFAESGOVYFG 229
                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA 7:193-201(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 85242112.
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 88224564.
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                                                                                                                                                                                                                                                                                                                                                      TNF OR TNFA.
                                                                                                                                                                                                                                                                                TNFA_MOUSE
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                                 Matches
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Baeyens K.J., De Bondt H.L., Raeymaekers A., Flers W., De Ranter C.J., "The structure of mouse tumour necrosis factor at 1.4 A resolution:
                                                                                                                                                               Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.; "Nucleotide sequence of the murine TNF locus, including the TNF-alpha (tumor necrosis factor) and TNF-beta (lymphotoxin) genes."; Nucleic Acids Res. 15:9083-9084 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               towards modulation of its selectivity and trimerization.";
Acta Crystallogr. D 55:772-778 (1999).
-!- FUNCTION: TWE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMPR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT A ACTION OF BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            propeptide results in a larger, inactive form of secreted protein.";
J. Biol. Chem. 264:16256-16260(1989).
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CTS, AND NOD;
MEDLINE; 96013654.
Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.
Takekawa K., Oghinara T.;
"Identification of a new susceptibility locus for insulin-dependent diabetes mellitus by ancestral haplotype congenic mapping.";
J. Clin. Invest. 96:1936-1942(1995).
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SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS EXTRACELLULAR SOLUBLE FORM.
PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 88165056. K. Albert I., Lu S.D.; Kriegler M., Perez X., Defay K., Albert I., Lu S.D.; M. A novel form of TNE/cachectin is a cell surface cytotoxic transmembrane protein: ramifications for the complex physiology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sherry B., Juc D.-M., Zentella A., Cerami A.; "Characterization of high molecular weight glycosylated forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alternative cleavage of the cachectin/tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               murine tumor necrosis factor.";
Biochem. Biophys. Res. Commun. 173:1072-1078(1990).
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NE; 99190964.
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Khim. 13:701-705(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beutler B.;
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                                                                           SEQUENCE FROM N.A.
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MEDLINE;
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        Bioorg.
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                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@15b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; FINE TO THE ALFORM.
PROSITE: PRO1235; TNFALFORM.
PROSITE: PS50049; TNF_2; 1.
PROSITE: PS50049; TNF_2; 1.

CYLOKINE; CYLOLOXIN; Transmembrane; Glycoprotein; Signal-anchor.
PROPEP 1 77 S33 TUMOR NECROSIS FACTOR.
77 S133 TUMOR NECROSIS FACTOR.
56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                    MOLITEMATOR THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE FUNCTION: THE IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN I SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 IVGPQR--FSGAPAMMEGSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSSWY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 VIGPQREEFPKDPSLI--SPLAQAVRSSSRTPSDKPVVHVVAN----PQAEGQL---QWL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YEPIYLGGVFQLEKGDRLSABINL 214
                                                                                                                                                                                                                                                                                                                                             BY GENERAL ILL HEALTH
                                                                                                                                                                                                                                  SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS
EXTRACELLULAR SOLUBLE FORM.
                                    Haudek S.B., Redl H., Schlag G., Giroir B.P.;
"Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL-----M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 VYVVK----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 233;
                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                      PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTECLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                             DISEASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                       DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF CANCER AND INFECTION, AND IS CHARACTERIZED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.6%; Score 143.5; DB ]
25.1%; Pred. No. 6.1e-05;
ive 38; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF019963; AAC31675.1; -.
INTERPRO; IPR000478; -.
INTERPRO; IPR002959; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM, PF00229, TNF, 1.
PRINTS, PR01234, TNECROSISFCT.
PRINTS, PR01235, TNFALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P33620;
01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 PSLLD-PDQDATYFG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                              AND MALNUTRITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | || : |||
|PDYLDFAESGQVYFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 49; Conserv
   SEQUENCE FROM N.A. MEDLINE; 98147379.
                                                                                                                                                                                                                    CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
TNFA_PAPSP
ID TNFA_PAPSP
                                                                         alpha.";
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   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQVLFK----GQGCPDYV-LLTHTVS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 RFAISYQEKVNLLSAVKSPCPKDTPEGAELKPW-----YEPIYLGGVFQLEKGDQLSA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 IVGPQRF----SGAP---AMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLS- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio hamadryas ursinus (Chacma baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01234; TNECROSISFCT.
PRINTS; PR01235; TNFALPHA.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMON NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
TNF OR TNFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .).
G -> R (IN REF. 3 AND 4).
16DD2A9676D68C5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%; Score 146.5; DB 1
25.6%; Pred. No. 3.5e-05;
iive 36; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA
                                               CAZ6457.1; -. AAA40462.1; ALT_SEQ. AAA40469.1; -. BAA19512.1; -. BAA19512.1; JOINED. BAA19513.1; JOINED. BAA19513.1; JOINED. BAA19513.1; JOINED. BAA19513.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MΨ;
                AAA40458.1; -. CAA68530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 QVSNPSLLD-PDQDATYFG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 EVNLPKYLDFAESGQVYFG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25895
AAA40457.1;
                                                                                                                                                                                                          PIR; A23127; QWMSN.
PIR; A22908; A22908.
PIR; A22908; A22908.
PIR; A27303; A27303.
PIR; A34251; A34251.
PIR; S03791; S03791.
PDB; ZTNF; 12-0CT-99.
MGD; MGI:104798; TNF.
INTERPRO; IPRO00295; -
PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 25.6
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
231
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235
56
179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36
148
186
231
235 AA;
                                                   X02611;
M20155;
M38296;
                                                                                                     D84196;
D84194;
                                                                                                                                                                             D84197;
D84198;
                                                                                                                                          D84195;
D84199;
                                 Y00467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFA_PAPHU O77510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                  EMBL;
EMBL;
                                   EMBL;
                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                            EMBL;
                                                                                                       EMBL;
                                                                                                                         EMBL;
                                                                                                                                                          EMBL;
                                                                                                                                                                             EMBL;
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                                                                                                                                          EMBL:
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음 ŏ q ò g ŏ qq 11;

Gaps

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11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.

TUMOR NECROSIS FACTOR.
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
MYRISTATE (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
BY SIMILARITY.
455360B48DC74173 CRC64;
                                                                                                                                           SUBUNIT: HOMOTRIMER.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.6%; Score 143.5; DB 1; Length 233;
25.6%; Pred. No. 6.1e-05;
tive 36; Mismatches 70; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL-----M 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 VYVVK----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSN 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IVGPQR--FSGAPAMMEGSWLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSSWY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFK----GQGCPSTHVLLTHTISRIAV 161
                                                     Papio sp. (Baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO1234; TNECROSISECT.
PRINTS; PRO1235; TNEALPHA.
PROSTE: PSO0251; TNE_1; 1.
PROSTIE; PSSO049; TNE_2; 1.
Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                  'PROTEOLYTIC PROCESSING.
                                                                                                                                                                                                                                                                                                                   -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TUMÓR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 BY
233 TC
56 SI
19 MY
20 MY
20 MY
25557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X62141; CAA44068.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 25.69
Matches 50, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSLLD-PDQDATYFG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P01375; 1TNF.
INTERPRO; IPR000478; -.
INTERPRO; IPR002959; -.
PFAM; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S22052; S22052.
                                                                                                                   [1] |
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                CONDITIONS
                                             TNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myristate.
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SEQUENCE
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                                             OR
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Db 215 PDYLDFAESGQVYFG 229

Search completed: December 29, 2000, 09:04:18 Job time: 48342 sec

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GenCore version 4.5
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protein search, using sw model OM protein -

; Search time 601.22 Seconds December 28, 2000, 19:38:02 Run on:

(without alignments) 49.077 Million cell updates/sec

US-08-989-362-2 Title: Perfect score:

1 MRRASRDYGKYLRSSEEMGS.....LLDPDQDATYFGAFKVQDID 316 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

297973 seqs, 93374136 residues Searched:

Total number of hits satisfying chosen parameters:

297973

length: 0 length: 2000000000 sed Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_14:* Database

sp_archa:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:* sp_vertebrate:* sp_mhc:*
sp_organelle:* sp_rodent:* sp_virus:* sp_mammal:* sp_plant:* sp_phage: * 10: 11: 12: 13: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

					SUMMARIES	
Result No.	Score	& Query Match	å Query Match Length DB	DB	ID	Description
г	1675	100.0	316	11	035235	O35235 mus musculu
7	1646.5	98.3	313	11	Q9R1Y0	O9rly0 mus musculu
m	1417.5	84.6	317	4	014788	014788 homo sapien
4	164	9.6	260	9	097605	097605 felis silve
5	154	9.5	260	9	097626	097626 canis famil
9	149	8.9	234	9	Q9TTJ3	09tti3 equus cabal
7	148	8.8	232	11	035853	035853 mus musculu
œ	146.5	8.7	239	11	оэохнэ	Q9qyh9 mus musculu
σ	145	8.7	260	11	Q922V2	Q9z2v2 rattus norv
10	145	8.7	260	11	Q9R254	Q9r254 rattus norv
11	142	8.5	232	4	Q9UIV3	Q9uiv3 homo sapien
12	140	8.4	174	4	095150	095150 homo sapien
13	139	8.3	234	9	Q28320	Q28320 capra hircu
14	134.5	8.0	240	4	043557	043557 homo sapien
15	133.5	8.0	233	9	018779	018779 bos taurus
16	133	7.9	157	4	043647	043647 homo sapien
17	132	7.9	149	9	097543	097543 actus nancy
18	131	7.8	149	9	097538	097538 actus vocif
19	131	7.8	149	9	O9TTG8	O9tta8 actus nigri

075476 homo sapien 070332 mesocricetu 09tt47 macropus eu 09tt97 aotus lemur 09ts98 us scrofa 09ts48 macropus eu 076737 dictyosteli 054907 mus musculu 09w990 marmota mon 045692 caenorhabdi 09v592 drosophila 091717 xenopus lae 09u592 drosophila 09u592 homo sapien 094450 homo sapien 09ts97 caenorhabdi 09uks8 homo sapien	Q03463 hepatitis c Q9rr94 deinococcus
4 075476 6 09TT47 6 09TT47 6 09TT47 6 09TT67 6 09TT67 11 09WV90 11 09WV90 11 09WV90 11 09WV90 12 091717 13 091717 14 09167 6 09TT12 6 09TT12 7 09365 6 09TT12 6 09TT12 7 09WVS8 8 09VKS8 8 09VKS8 10 091619 10 092008 10 092008 10 090080	12 Q03463 2 Q9RR94
240 216 216 386 138 3848 225 169 169 169 93 294 891 891 205 616 616 750 355	3011
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130.5 1126.5 1126.5 1126.5 100.5 100.03 102.03 102.03 99.5 99.5 92.5 92.6 93.6 93.6 94.6 95.6 96.7 97.6 97.6 97.6 97.6 97.6 97.6 97	06 88 88
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ALIGNMENTS

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Choi Y.;
"TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells.";
J. Biol. Chem. 272:25190-25194(1997).
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Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki M.,
Mochizuki S.-H., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,
                                                                                                                                                                                                                                                  TISSUE=HYBRIDOMA;
MEDLINE; 97460112.
Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=BONE MARROW;
MEDLINE; 98227661.
Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
            035235, 035306;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL) (TRANCE) (OPGL)
(OSTBOROTEREERIN LIGAND) (TUMOR NECROSIS FACTOR LIGAND) (ODF).
TNF-SFIL OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyle W.J., "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation.",
   AA
   PRT;
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SEQUENCE FROM N.A.
IISSUE-BONE MARROW STROMA;
   PRELIMINARY;
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SEQUENCE FROM N.A.
035235
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Q9R1Y0
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                                                                                                                                     "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function.";
Nature 390:175-179(1997).
-!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.; "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
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                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
-!- TISSUE SPECIFICITY: HIGHER LEVELS IN THE BONE MARROW AND STROMAL CELLS THAN SPLEEN, THYMUS AND LYMPH NODE.
-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS PACTOR FAMILY.
EMBL; APO53713; AAC40113.1; -.
EMBL; ABO08426; BAA5425.1; -.
EMBL; AF019048; AAB86812.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VILSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
G -> D (IN REF. 4).
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                                                                                                    Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D., Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1675; DB 11; Length 316; 100.0%; Pred. No. 1.5e-147; tive 0; Mismatches 0; Indels 0;
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08DF63A2BE00967A CRC64;
                                              Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998)
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197 197
262 262
99 99
316 AA; 34944 M
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INTERPRO; IPR000478; -.
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                                                                   SEQUENCE FROM N.A.
TISSUE=THYMIC LYMPHOMA;
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69
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                                                                                          MEDLINE; 98032977.
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Best Local $
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61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDTLPDSCRRMKQ 120
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                                                                                                                                                                                                                                                                                                 Ueda M., Higashio K.; "Cloning and characterization of the gene encoding mouse osteoclast differentiation factor."; Gene 230:121-127(1999).
                                                                                                                                                                                                                                                   STRAIN=129;
Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVY
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
1TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL) (TRANCE) (OPGL)
(OSTEOPROFECERIN LIGAND) (TUMOR NECROSIS FACTOR LIGAND).
THESFIL OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 98.3%; Score 1646.5; DB 11; Length 313; Best Local Similarity 99.1%; Pred. No. 6.4e-145; Matches 313; Conservative 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NE_2; 1.
34719 MW; 37D530B8BFC2842E CRC64;
                                                                       Last sequence update)
Last annotation update)
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313
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TISSUE-BONE MARROW, AND PERIPHERAL BLOOD;
                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                EMBL, AB022039; BAA36970.1; -.
EMBL, AB022036; BAA36970.1; -.
EMBL, AB022037; BAA36970.1; JOINED.
EMBL, AB022038; BAA36970.1; JOINED.
INTERPRO; IPR000478; -.
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                                                                                                                OSTEOCLAST DIFFERENTIATION FACTOR
                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
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PROSITE; PS50049; TNF_
SEQUENCE 313 AA; 34
                                                                                                                                        Mus musculus (Mouse).
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SEQUENCE FROM N.A.
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-!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR. AUGMENTS ABILLTY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
                                             "A homologue of the TNF receptor and its ligand enhance T-cell growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQDSTLESEDT--LPDSCRRM 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
(POTENTIAL).
                                                                                                                                    Lacey D.L., Timms.E., Tan H.-L., Kelley M.J., Dunstan C.R., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.;
                                                                                                                                                                                                                                                                                                                                                                                            PROLIFERATION.
--- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
--- TISSUE SPECIFICITY: HIGHERAL BLOOD LEUKCKTIES, BONE MARROW, HEART, WEAK IN SPLEETAL WGSZIE, STOMACH AND THYROLD.
--- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
EMBL; AF019047; AAB68911.1; --
EMBL; AF013171; AACS1762.1; --
EMBL; AF013171; AACS1762.1; --
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                                                                                                                                                                                                                                                                                            Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M., Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPAPAASRSMFLALLGLGLGQ
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N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                   "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."; Cell 93:165-176(1998).
           Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
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84.3%; Pred. No. 1.2e-123;
ive 16; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00229; TNF; 1.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
                                                             and dendritic-cell function."; Nature 390:175-179(1997).
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                                                                                                                                                                                                                                                      SEQUENCE OF 73-317 FROM N.A. TISSUE=THYMOCYTES;
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317 AA;
98032977.
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                                                                                                               TISSUE=LYMPH NODE;
MEDLINE; 98227661.
                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor.
                                    Galibert L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sim
Matches 268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                    Choi Y
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RILRLHENAGLQDSTLESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 VFMKTLQKCNKGEGALSLL----NCEEIKSRFE-AFLKEIMLNKETKKEKNV----- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 APSAPAPAPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCF--Y 89
9 APRSVAPGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLDK---IEDERNLYEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--MTLSNGK-LR
                                                                                     VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 VNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--LMKGGSTKNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 SGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.8%; Score 164; DB 6; Length 26
24.6%; Pred. No. 1.9e-07;
.ive 53; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hosia M.J., Willett B.J.;
"Adjuvant properties of feline CD154 (CD40 ligand).";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF0791015, AAD02954.1;
HSSP; P29965; IALY.
INTERPRO; IPR000478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : | | ::| | : | | : | | : | | : | | SSSKPCGQQSIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM: PF00229; TNF: 1.
PROSITE; PS00251; TNF_1: 1.
PROSITE; PS50049; TNF_2: 1.
SEQUENCE 260 AA: 28727 MW; 349FA0391FB7B932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD154.
Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae,
                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                           260 AA
                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DOMESTICUS; TISSUE=THYMUS;
                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-2000 (TrEMBLrel. 13, CD40 LIGAND.
                                                                                                                                                                           299 DPDQDATYFGAFKVQDID 316
                                                                                                                                                                                                 300 DPDQDATYFGAFKVRDID 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 24.6*
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              097626
097626;
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Query Match
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035853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 VFMKTLQKCNKGEGSLSLL----NCEIKSQFE-AFLKEIM-LNNEMKKEENIAM---- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISN--MTLSNGK-LR 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNQDGFYYLYANICF-RHHETSGSVPTDYLQLMVYVVKTSIKIPSSHN--LMKGGSTKNW 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 VKRQGLYYVYAQVTFCSNRAASSQAP-----FVASLCLHSPSGTERVLLRAASSRGS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 APSAPAPAPPAASRSMFLALLGLGLGQVVCSIALF-LYFRAQMDPNRISEDSTHCF--Y 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----QKGDQDPRIAAHVISEASSNPA----SVLRW-APKGYYTISSNLVSLENGKQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishida N., Sato F., Hasegawa T.;
"Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB035735; BAA88349.1;
INTERPRO; IPR000478;
INTERPRO; IPR00259;
INTERPRO; IPR0025969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S---GNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 SKPCGQQ-----SIHLGGVFELHPGASVFVNVTDPSQVSHGTGFTSFGLLKL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%; Score 154; DB 6; Length 26
Best Local Similarity 24.7%; Pred. No. 1.6e-06;
Matches 72; Conservative 54; Mismatches 114; Indels
                                                                                                                                             Hosie M.H., Willett B.J.;
"Adjuvant proporties of canine CD40L.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBE; AF086711; AAD04375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01234; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
PRINTS; PR01235; TNFALPHA.
PRINTS; PR01235; TNFALPHA.
PROSITE; PS00251; TNF_1: 1.
PROSITE; PS50049; TNF_2: 1.
SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;
                                                                                                                                                                                                                                                                     INTERPRO; IPRO00478; -.
PFAM; PE00229; TNF; 1.
PROSITE; PS0521; TNF_1; 1.
SEQUENCE 260 AA; 28688 MW; 604F69A19E98EB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
TUMOR NECROSIS FACTOR-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-THOROUGHBRED; TISSUE-ARTERIAL ENDOTHERIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                    Canis familiaris (Dog)
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150
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Q9TTJ3
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DDT AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 SYQEKVNLLSAVKSPCPKDTPEGAELKPW------YEPIYLGGVFQLEKGDQLSAEVNL 213
                                                                                                                                                                                                                                                                                                                                    S5 VIGPQREEQLPNARQ-SINPLAQTLRSSSRTPSDKPVAHVVAN----PQAEGQL---QWL 106
                                                                                                                                                                                                                             107 SGRANALLANGVKLTDNQLVVPLDGLYLIYSQVLFK----GQGCPSTHVLLTHTISRLAV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 IVGPQR---FSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLS-SWYH 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 -----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSN 294
                                                                                                  133 IVGPQRFSGAPAMMEGSWLDVAQRGK-----PEAQPFAHLTINAASIPSGSHKVTLSSWY 187
                                                                                                                                                                                                                                                                                                      247 KIPSSHNLMKG------GSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSN 294
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 DRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVK----
                                                                                                                                                                                                    188 HDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Iraqi F., Teale A.; "Cloning and sequencing of the tnfa genes of three inbred mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40;
                                                      38;
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     Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenetics 45:459-461(1997).
EMBL: U68414; AAB55593.1; -
EMBL: U68414; AAB55593.1; -
HSSP; POI375; 4TSV.
INTERPRO; IPR002959; -
PRAM; PP00229; TNF: 1.
PRINTS; PR01234; TNF=CSISECT.
PRINTS; PR01235; TNFALPHA.
PROSITE; PS00245; TNF=2; 1.
SEQUENCE 232 AA; 25513 MW; 2ED6DA8EODCAADD8 CRC64;
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                                                      72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
  Score 149; DB 6;
Pred. No. 4.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 148; DB 11; Pred. No. 5e-06; 34; Mismatches 7
Query Match 8.9%; Score 149; DE Best Local Similarity 24.1%; Pred. No. 4.1e Matches 47; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAY-2000 (TrEMBLrel. 13, TUMOR NECROSIS FACTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          295 PSLLD-PDQDATYFG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 PSLLD-PDQDATYFG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                         216 PNYLDFAESGOVYFG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 PKYLDFAESGOVYFG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 97246744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A/J;
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-----EKKEKSF--EMQKGDEDPQIAAHVVSEA-----NSNAASVLQWAKKGYYTM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 SERILLRAANTHSSSKLCEQQ--SIHLGGVFELQAGASVFVNVTEASQVIHGIGFSSFGL 257
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CD40 LIGAND.
Ratus norvegicus (Ratl).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                  91 ILRLHE------KELQDSTLESEDTLPDSCRRMKQAFQGAVQ----KELQHIV 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LHEDFVFVKKLKRCNKGEGSLSLL-----NCEEMRRQFEDLVKDISLNKE---- 103
                                                                                                                                                                                                                                                 32 PAPSAPAPAPAPASRSMFLALLGLGL-GQVVCSIALFLYFRAQMDPNRISEDSTHCFYR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAPSAPAPAPAPASRSMFLALLGLGL-GQVVCSIALFLYFRAQMDPNRISEDSTHCFYR 90
                                                                                                                                                                                                                                                                             ---LHEDFVFVKKLKRCNKGEGSLSLL-----NCEEMRRQFEDLVKDISLNKE----
                                                                                                                                                                                                                                                                                                                                                                                                                 135 GPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 ISNM-TLSNGK-LRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 N---LMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72;
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                                                                                                                                                                      Length 260;
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Hallett K.M., Oaks M.K.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF116582; AAD22460.1; -.
INTERPRO; IPR000478; -.
PFAM; PF00229; TNF; 1.
PROSITE; PS000251; TNF_1; 1.
PROSITE; PS000251; TNF_1; 1.
SEQUENCE 260 AA; 29259 MW; B3D3757DE60DB73A CRC64;
HSSP; P27548; 1CDA.
INTERPRO; IPR000478; -.
PFAM; PF00229; TNF; 1.
PROSITE; PS000251; TNF_1; 1.
PROSITE; PS00049; TNF_2; 1.
SEQUENCE 260 AA; 29282 MW; 15D21F5200F6DEBB CRC64;
                                                                                                                                                                  Query Match 8.7%; Score 145; DB 11; Best Local Similarity 24.4%; Pred. No. 1.1e-05; Matches 74; Conservative 54; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.7%; Score 145; DB 11;
25.1%; Pred. No. 1.1e-05;
ive 50; Mismatches 93;
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Best Local Similarity 25.19
Matches 72; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DYLQLMVYVVKTSIKIPSSHNLM-----KGGSTKNWSGNSEFHFYSINVGGFFKLRA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77; Gaps
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CD40 LIGAND.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                         TNF
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                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSG-SVP---T
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                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB-FETAL LIVER CELL;
Misawa K., Nosaka T., Kitamura T., Kojima T.;
"Murine LIGHT, a homologue of human LIGHT which is a member family.";
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STRAIN=PVG; TISSUE=SPLEEN;
Daniel K.C., Foss Y., Moussavi A., Macary P., Kemeny D.M.,
Farzaneh F., Gaken J.A.;
"Cloning and sequencing of rat CD40 ligand.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF013985; AAD09323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM. PF00229; TNF; 1.
PRINTS; PR01234; TNECROSISFCT.
PROSITE; PS50049; TNF_2; 1.
SEQUENCE 239 AA; 26338 MW; 217874AC71AD6BE3 CRC64;
                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 8.7%; Score 146.5; DB 11; Best Local Similarity 25.3%; Pred. No. 7.2e-06; Matches 68; Conservative 39; Mismatches 85;
                                                                                 239 AA
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                                                                               PRELIMINARY;
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Pennica D., Goeddel D.V., Gray P.W.;
                                                                                                                                                                                                                                                                                                                                                          Perrot V.,
                                                                                KSNLVVLENGRQLIVKREGLYYVYTQVTF----CSNREP---LSQRPFIVSLWLK-PSSG 199
                                                         ISNM-TLSNGK-LRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSH 252
          GPQRFSGAPAMMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLSSWYHDRGWAK 194
                                 -----EKKEKSF--EMQRGDEDPQIAAHVVSEA----NSNAASVLQWAKKGYYTM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
Wallace A.F., Russell M.E.;
"Allograft inflammatory factory-1. A cytokine-responsive macrophage
molecule expressed in transplanted human hearts.";
Transplantation 61:1387-1392(1996).
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                                                                                                                                                                                                                                                                                                                                                         Iris F., Bougueleret L., Prieur S., Caterina D., Primas G., Perrot Unrka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.; "Dense Alu clustering and a potential new member of the NF kappa B family within a 90 kilobase HLA class III segment.";
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chow B.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.; "Lymphotoxin beta, a novel member of the TNF family that forms heteromeric complex with lymphotoxin on the cell surface."; cell 72:847-856(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human lymphotoxin and tumor necrosis factor genes: structure, homology and chromosomal localization."; Nucleic Acids Res. 13:6361-6373(1985).
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                                                                                                          N---LMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPS 296
                                                                                                                        SERILLRAANTHSSSKLCEQQ--SIHLGGVFELQAGASVFVNVTEAS 244
                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                              232 AA
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                                                                                                                                                                                              PRT;
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tmmunogenetics 42:315-322(1995).
                                                                                                                                                                                                                    (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 14,
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                                                                                                                                                                                                                                                                                 sapiens (Human).
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Shina T., Tamiya G., Oka A., Yamagata T., Yamagata N., Kikkawa E.,
Shina T., Tamiya G., Oka A., Fukuzumi Y., Taguchi S., Sugawara C.,
Ono A., Chen L., Yamazaki M., Tashiro H., Ando A., Ikemura T.,
Kimura M., Inoko H.;
"Nucleotide sequencing analysis of the 146-kilobase segment aroud the
IkBL and MICA genes at the centromeric end of the HLA class I
                                                                                                                                                                                                                                                                                                                                                        "Characterization of a novel gene in the human major
histocompatibility complex that encodes a potential new member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | :: | :: | :: | 104 LNRRANALLANGVERENDNQLVVPSEGLYLIXSQVLFK----GQGCPSTHVLLTHTISRIA 159
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Van Zeveren A., Coppieters W., Van de Weghe A., Bouquet Y., Choy W.,
Strominger J., Spies T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MVYVVK----TSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differential regulation, initiation, and alternative splicing."; Genomics 45:591-600(1997).
                                                                                                                                       Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S., "Haplotypic polymorphisms of the TNFB gene.";
Immunogenetics 33:50-53(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complex expression patern of the TNF region gene LST1 through differential regulation, initiation, and alternative splicing."
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Weiss E.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neville M.J., Campbell R.D.; Alternative splicing of the LST-1 gene located in the major "Alternative splicing of the LST-1 gene located in the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 YHDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        histocompatibility complex on human chromosome 6."; DNA Seq. 8:155-160(1997).
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; Pred. No. 1.8e-05;
37; Mismatches 69.
                                                                                                                                                                                                                                                                                                                                                                                                            I kappa B family of proteins.";
Hum. Mol. Genet. 3:793-799(1994).
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PRINTS; PR01234; TNECROSISFCT.
PRINTS; PR01235; TNFALPHA.
PROSITE: PS00251; TNF_1; 1.
PROSITE: PS50049; TNF_2; 1.
SEQUENCE 232 AA; 25446 MW; I.
level of TNF-beta production.";
J. Exp. Med. 173;209-219(1991).
                                                                                                                                                                                                                                                                                                                                Albertella M.R., Campbell D.R.;
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Best Local Similarity 24.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 47:372-382(1998).
EMBL; X14768; CAA75070.1; -
INTERPRO; IPR000478; -.
INTERPRO; IPR002959; -.
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                                                                                         SEQUENCE FROM N.A. MEDLINE; 91139175.
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                                                                                                                                                                                                                                                                                                    MEDLINE;
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Query Match
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160 VSYQTKVNLLSAIKSPCQRETPEGAEAKPW-----YEPIYLGGVFQLEKGDRLSAEIN 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 WYHDRGWAKISN-MTLSNGKLRVNQDGFYYLYANICFRHHETSGSV-----PTDYLQLM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 VYVVKTSIKIPSSHNLMKGGST----KNWSGNSEFHFYSINVGGFFKLRAGEEISIQVS 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=VASCULAR ENDOTHELIAL;
Yu G. L., Zhai Y., Ni J., Iruela-Arispe L., Huang W.-Q., Xing L.,
Lu J., Kozak D., Jiang G.-W., Rojas L., Janat M.F., Buergin M.,
Gentz S., Lippman M.E., Aggarwal B.B., Ruben S., Gentz R., Li L.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNF-ALPHA.
Capra hircus (Goat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu G.-L.;
"A Novel-Endothelial Cell-Specific Negative Regulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF039390; AAD08783.1; -.
HSSP; P01375; 1A8M.
INTERPRO; IPPO478; -.
PRAM: PF00229; TNF: 1.
PRINTS; PR01234; TNECROSISFCT.
PROSITE: PS50049; TNF_2: 1.
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                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
VASCULAR ENDOTHELIAL CELL GROWTH INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                       174 AA
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                                                                                                                                                                                                                                                                                                                       PRT;
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155 DISLVDYTKEDKTFFGAF 172
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Best Local Similarity 28.33
Matches 39; Conservative
                                                                  294 NPSLLD-PDQDATYFG 308
                                                                                                              | || : |||
213 RPDYLDFAESGOVYFG 228
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                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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028320
AC 028320
DT 028320
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DT 01-NOV
DT 01-NOV
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OC MAMMAIY
OC MAMMAIY
OC MAMMAIY
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RT TARARU
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INTERPRO: IRF000478: -. PFAM; PF00229; TNF: 1. PROSITE; PS50049; TNF: 2: 1. SEQUENCE 240 AA; 26351 MW; 49D0BF67E1390B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
Ware C.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ETSGSVPTDYLOLM 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 VNIL-SAIKSPCHRETPEGAEAKPW-----YEPIYOGGVFQLEKGDRLSAEINOPEXL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 IVGPQRFSGAPAMME-GSWLDVAQRGKPEA---QPFAHLTINAASIPSGSHKVTLSSWYH 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 AVQGWFLLQLHWRLGEMVTRLPDGPA---GSWEQLIQERRSHEVNPAAHLT-GANSSLTG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 SHKVTLSSWYHDRGWAKISNWTLSNGKLRVNQDGFYYLYANICFRHHETSG-SVPTDYLQ 236
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 VYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33;
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                                                                                                                                                                                                                                                                                                                   Length 234;
                                                                                                                                                                                                                                                                                                                                                                          82; Indels
                                                                                                                                                                                                                                    9768E33BBBABB041 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                 8.3%; Score 139; DB 6;
25.7%; Pred. No. 3.5e-05;
tive 30; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER LIGHT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 DRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHH-
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                                        INTERPRO; IPPO00478; -
INTERPRO; IPPO0039; -
FPAM; PPO0229; TWF; I.
PRINTS; PR01234; TNFCROSISECT.
PRINTS; PR01235; TNFALPHA.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS0029; TNF 25; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06,
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D86587; BAA13130.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 28.59
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 D-PDQDATYFG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 DYAESGQVYFG 230
                        P01375; 4TSV
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                      133 IVGPQR--FSGAPAMMEGSWLDVAQRGKPEA---QPFAHLTINAASIPSGSHKVTLSSWY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 QLRWWDSYANALMANGVKLEDNQLVVPPADGLYLIYSQVLFRGQGCPSTPLFLIHTISRIA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 VSY-QTKVNIL-SAIKSPCHRETPEWAREAKPW-----YEPIYQGGVFQLEKGDRLSAE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 HDRGWAKISNMTLSNG-KLRVNQ-----DGFYYLYANICFRHH------ETSGSVP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 TDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQ 291
                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

8.0%; Score 133.5; DB 6; Length 233;
Best Local Similarity 25.8%; Pred. No. 0.00011;
Matches 51; Conservative 30; Mismatches 72; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   | Iraqi F.:
| Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. |
| RMSL; AF011926; AAB84086.1; -. |
| RMSP; P01375; 4TSV. |
| RMSEPRO: IPR002959; -. |
| RTERPRO: IPR002959; -. |
| R PEAM; PF00229; TNF. 1. |
| R PEAM; PF00229; TNF. 1. |
| R PRINTS; PR01234; TNECROSISFCT. |
| R PRINTS; PR01235; TNFALPHA. |
| R PROSITE; PS00251; TNF 1; 1. |
| PROSITE; PS0049; TNF_2; 1. |
| SEQUENCE 233 AA; 25395 MW; 8D8729025DE516B0 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TUMOR NECROSIS FACTOR ALPHA.
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                                                                     287 EISIQVSNPSLLD-PDQDATYFGAFKV 312
                                                                                                                                                                                                      PRT;
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AW104932 x177401_x1 NCI_CGAP_PT
AW104932 x177401_x1 Scares_preq
AA298009 EST11364 T-cent_1 ymph
AIG-8285 fc12f06_y1 zebrafish W
BE000089 MR0-BN0070-200400-015-
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A4444493 ne38f03 x1 Soares_Diec
A4444493 ne38f03 x1 NCI CGAP_CC
H44565 yo75h09.1x1 NCI CGAP_CC
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A1798802 we92h03.x1 Soares_NFL
A1524976 promrna-2.E01.r bytumC
BE457735 us96e01.x1 Soares_Lhym
H54629 yq91a1.s1 Soares_Lhym
H54629 yq91a1.s1 Soares_Elah
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AL183238 Tetraodon nigroviridis
236726 HHEA47M Atrium cDNA libi
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AA291356 zt44c07.r1 Soares ovar
H43566 yo64h10.r1 Soares breast
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AI982044 pat.pk0072.c9.f chicke
AI253279 ESTRB0004 SuperScript
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AW838386 QV2-LT0053-020400-119-
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AW025893 wv71d09.xl Soares_thym
                                                                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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AW607607 MR3-HT0487-290100-1
H44567 y075110.rl Soares bre
H4772 yp20e12.rl Soares bre
A1410040 EST238333 NOTMA11ze
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3887
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
Plate: 832 row: F column: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Holzman,T.,
Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 524)
                                                                                                                                                                      seq_documentation_block:
LOCUS AQ827122 524 bp DNA GSS 27-AUG-1999
DEFINITION HS_2256_B2_C09_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=832 Col=18 Row=F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mahairas,G.G., Waliace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Plate=832 Col=18 Row=F"
/clone_lib="RPCI-11 Human Male BAC Library"
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Gaps: 0
Percent Identity: 81.111
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c 99 g 151 t
0.7965
2.22
2.61
4.39
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Location/Qualifiers
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            175.78
167.78
166.52
162.46
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                                                                                                                                                                                                                                                                           AQ827122
AQ827122.1 GI:5793184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
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Ratio: 4.578
                                                                                                                                  seq_name: gb_gss12:AQ827122
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us-08-989-362-2.rst

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LOCUS
BE042463
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                                                                                                                                                     Percent Similarity:
                                                                                                                        Ratio:
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 529)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L.
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-38887
Fax: (206) 616-38887
Fax: (206) 616-38887
Fax: (206) 616-3887
Fax: (206) 616-38887
Fax: (206) 616-3887
Fax: (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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LOCUS AQ827166 529 bp DNA GSS 27-AUG-1999
DEFINITION HS_5256_B2_G09_T7A RPI-11 Human Male BAC Library Homo sapiens
genomic clone plate=832 Col=18 Row=N, DNA sequence.
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99380589
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/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                 6 others
417, CCTAGTATTGGTCAGGAAATTATGAATTCCATTTTATTATTCCATAAACGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 CAACCCCTCCTTACTGGATCCGGATCAGGATGCAACATACTTTGGGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                       rAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyAlaP
                                                                                                                                              260, hrLysAsnTrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnVal
                                                                                                                                                                                                                                                                                         277 GlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIleGlnValSe
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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Plate: 832 row: N column: 18
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AQ827168.1 GI:5793230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 TTAAAGTTCGAGATATAGAT 248
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ORIGIN
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COMMENT
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenh.gov
Email: Robert_Strausbergenh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrapad by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_CO14"
/tissue_type="moderately-differentiated adenocarcinoma"
/tissue_type="moderately-differentiated adenocarcinoma"
/tissue_type="moderately-differentiated adenocarcinoma"
/tissue_type="moderately-differentiated adenocarcinoma"
/note="Organ: colon; Vector: pcMV-SPORT6; Site_1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE042463 618 bp mRNA EST 08-JUN-2000 ho22c06.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:3038122 similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 luPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgAla 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspProAs 301
                                                                                                                                                                                                                                                                                                                         251 rHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 GGAGAGGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACTGGATCCGGA
                                                                                                                                                                                                                                                                                         LeuGlnLeuMetValTyrValValLysThrSerIleLysIleProSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                454 TCATACCNTGATGAAAGGAGCAAGCACCAAGTATTGGTCAGGGAATTCTG
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Gaps: 1
Percent Identity: 78.049
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Location/Qualifiers
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                                                                                                                                                                                                                           to reverse of: AQ827168
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BE042463
BE042463.1 GI:8359516
                                                                                                                                                            US-08-989-362-2 x AQ827168/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
Unpublished (1997)
                                                                 90.244
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   315.50
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BASE COUNT ORIGIN

Gay, C., Holt and

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                         Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray lopublished (2000)

Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
                                                                    1 (bases 1 to 683)
Hegde, P., Qi.R., Abernathy, K., Dharap, S., Gaspard, R.,
J.E., Saedd, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. a
Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 ThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIl 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGAATATTTGAG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 LeuArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLe 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACTTGAGGAATGGTGAACTGGTCATCCATGAAAAAGGGTTTTACTACA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 euTyrAlaAsnIleCysPheArgHisHisGluThrSerGlySerValPro 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 ATARARCTCCTGGGAATCATCAAGGAGTGGGCATTCATTCATTCCTGAGCAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 131
Gaps: 2
Percent Identity: 35.878
                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone_llb="MAGE resequences, }
/note="Vector: pBluescript5Km"
125 c 124 q 174 t
                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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to:
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Plate: 5
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2.407
69.466
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US-08-989-362-2 x AW949689
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        ORGANISM
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ORIGIN
                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                              JOURNAL
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                                                                                                                                                     TITLE
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Average insert size 1.7 kb. Life Technologies catalog #: 11531-019"
                                                                                                                                                                                                                                                                                                                                 127 GlnLysGluLeuGlnHisIleValGlyPro......GlnArgPheSe 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 IleProSerGlySerHisLysValThrLeuSerSerTrpTyrHisAspAr 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alAsnGlnAspGlyPheTyrTyrLeuTyrAlaAsnIleCysPheArgHis 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 TCCATGAAAAAGGGTTTACTACATCTATTCCCAAACATACTTTCGATT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 HisGluThrSerGlySerValProThrAspTyrLeuGlnLeuMetValTy 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :::||| :::||| 363 CAGGAGAATAAAAGAAAAACACAAAGAACGACAAAATGGTCCAATA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 rValValLysThrSerIleLysIleProSerSerHisAsnLeuMetLysG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 GIGCTAGAAATAGTIGTIGGICTAAAGAIGCAGAAIATGGACTCIATICC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307
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166 TTCTGTAACAAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTTT 117
                                                                                                                                                                                                                                                                                                                                                                                                                      140 rGlyAlaProAlaMetMetGluGlySerTrpLeuAspValAlaGlnArgG 157
                                            2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 IleAsnValGlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIl
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                                                                                                                                                                           Gaps: 4
Percent Identity: 30.688
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                                               222
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                                               9
                                            110
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US-08-989-362-2 x BE042463/rev
                                          125 c
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2.064
57.672
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LOCUS     AW949689
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                                            159
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                                                                                                                                                                                                                                                                                              Align seg 1/1
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497

190

207

358

DEFINITION

290

ACCESSION VERSION KEYWORDS SOURCE

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Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.
AW945165 718 bp mRNA EST 31-MAY-2000
EST361358 MAGE resequences, MAGA Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            Assessment of gene expression patterns in a model of colon tumor matastasis using a 19,200 element CDNA microarray Unpublished (2000)

Contact: John Quackenbush
THE Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrL 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 eProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerG 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGA"
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Percent Identity: 35.878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="MAGE resequences, Note="Vector: pBluescriptSKm" 136 c 130 g 179 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                            AW945165
AW945165.1 GI:8122916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: johnq@tigr.org
Plate: 0
                                                                                                                                                                                                        (bases 1 to 718)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: Reverse
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US-08-989-362-2 x AW945165
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                                                                                                                                    Homo sapiens
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Ratio:
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                                                                                                                  human.
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                    DEFINITION
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VERSION
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                                                                                                                                                                                                                             AUTHORS
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                                                                                        KEYWORDS
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                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                               SOURCE
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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3688

Fax: (206) 616-3887

Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 841 row: H column: 5
Seg primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 413)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                             AQ817650 413 bp DNA GSS 26-AUG-1999
HS_5265_B1_D03_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=841 Col=5 Row=H, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="fexon:9606"
/clone="Plate=841 Col=5 Row=H"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 gAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspP 300
Length: 50
Gaps: 0
Percent Identity: 82.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AQ817650 from: 1 to: 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 413.
Location/Qualifiers
                                                                                                                                                                                                                    AQ817650
AQ817650.1 GI:5780043
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92.000
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US-08-989-362-2 x AQ817650
                                                                      seq_name: gb_gss11:AQ817650
                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                    Homo sapiens
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/clone="Inba" NGI_CS97851"
/tissue_type="tumor, 5 pooled (see description)"
/tissue_type="tumor, 5 pooled (see description)"
/tab_host="Organ ovary; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ ovary; Vector: pCMV-SPORT6; Sall;
/note="Org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 405.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                           AW104819 585 bp mRNA EST 20-OCT-1999 xd57b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597851 similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                      105 CCGATCAAGATGCAACATACTTTGGGGCTTCTTAAGAGCGAGATATGGAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe 198
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                                                                    roAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                              LIGAND ;, mRNA sequence.
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Unpublished (1997)
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/Gev_stage="Adult"
/dev_stage="Adult"
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Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
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1 (bases 1 to 604)
1 (bases) to 604)
1 blass Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Printstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RCO-BN0121-210
300-031-e03&t3=2000-03-21&t4=1)
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RCO-BN0121-210300-031-e03 BN0121 Homo sapiens cDNA, mRNA sequence.
BE005955
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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20202663
                               232 ThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIl 248
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                                                                                                                                                                                                                                                                                281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282 LeuArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLe 298
euTyralaAsnIleCysPheArgHisHisGluThrSerGlySerValPro 231
                                                                                                                                                      265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys
                                                                                                                                                                                                                                       248 eProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerG
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/db_xref="taxon:9606"
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High quality sequence stop: 164
Location/Qualifiers
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profiles into the pUC 18 vector. Reverse transcription of trissue mRNA and cDNA amplification were performed under low stringency conditions.

120 c 131 g 148 t
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                                                                                                                                                                                                                                                                                                                                   117 ArgMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIl 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 laMetMetGluGlySerTrpLeuAspValAlaGlnArgGlyLysProGlu 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
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                                                                                                                                                                                                                                                                                                                                                                                                                  eVal......GlyProGlnArgPheSerGlyAlaProA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTATATGGTTGATGACAAGTGCTAGAAATAGTTGTTGGTCTAAAGATGC 454
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Percent Identity: 27.751
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to:
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                                                                                                                                                                           1.720
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                                                                                                                                                           199.50
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US-08-989-362-2 x BE005955
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LOCUS AA687481
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                                                                                                                                                           Quality:
                                                                                                                                                                                                Percent Similarity:
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                                                            202
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ORIGIN
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11-DEC-1997

EST

mRNA

452 bp

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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@ih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLORE distribution: NGI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: -Samils revl ET from Amersham
High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
76 c 79 g 119 t
                                                                                                                                                                                                                                                                            Eukaryotta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 452) NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          'n
ns58e08.rl NCI_CGAP_Pr22 Homo sapiens cDNA clone IMAGE:1187846 similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING LICAND;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 TyrTyrLeuTyrAlaAsnIleCysPheArgHisHisGluThrSerGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 TrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 rValProThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="normal prostate"
/lab_host="DH10B"
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                             AA687481
AA687481.1 GI:2675672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161.50
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US-08-989-362-2 x AA687481
                                                                                                                                                                                                                                                       Homo sapiens
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SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 502) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             x177d01.x1 NCI_CGAP_Panl Homo sapiens cDNA clone IMAGE:2680705 3'
similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING
LIGAND; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 euArgLeuHisGluAsnAlaGlyLeuGlnAspSerThrLeuGluSerGlu 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                        9 GlyLysTyrLeuArgSerSerGluGluMetGlySerGlyProGlyValPr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlnValValCysSerIleAlaLeuPheLeuTyrPheArgAlaGlnMe 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 oHisGluGlyProLeuHisProAlaProSerAlaProAlaProP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 roProAlaAlaSerArgSerMetPheLeuAlaLeuLeuGlyLeuGlyLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                           68 GGTGGGTACCTGCGTGGTGCCGCGGAGATACAGGTGACTCCT......
                                                                                                                                                                                     Percent Identity: 32.394
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11548-013
     μ.
                                                                                                                                    Length:
                                                                                                                                                                  Gaps:
     107
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Unpublished (1997)
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1.722
63.380
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LOCUS AW191932
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     Ø
                                                                                                                                    Quality:
                                                                                                                                                                                  Percent Similarity:
  111
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     BASE COUNT
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TITLE
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KEYWORDS
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                             ORIGIN
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                                                                                                                                                                                                                                                                                                                                             AW637373 456 bp mRNA EST 03-APR-2000 b157h07.wl Blackshear/Soares normalized Xenopus egg library Xenopus laevis cDNA clone PBX0057H07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 456)
Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman
, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEHS Xenopus Maternal EST Project
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone is available through Research Genetics, Inc., 2130 Memorial Barkway, UnitsVille, AL 35901 phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Blackshear/Soares normalized Xenopus egg
                                                                                                                                                       150 TGGTCTAAAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGAAT 199
                                                   279 ePheLysLeuArgAlaGlyGluGluIleSerIleGlnValSerAsnProS 296
                                                                                 :|||:::|||:::|||200 ATTTGAGCTTAAGGAAAATGACCAGAATTTTTGTTTTCTGTAACAAATGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus laevis"
/db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: CAGGAAACAGCTATGACC
Plate: 0057 row: H column:
Seq primer: 17 primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="PBX0057H07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW637373.1 GI:7394485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    African clawed frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .456
                                                                                                                                                                                                                                                              seq_name: gb_est23:AW637373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butherla; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 468)

NGI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1113 Std Error: 0.00

Seq primer: -40mi3 fwd. ET from Amersham High quality sequence stop: 390.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          468 TACATCTATTGCCAAACATACTTTCGATTGCAGGAGGAAATAAAAGAGAA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 TrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPh 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 ATTTGAGCTTAAGGAAAATGACAGAATTTTTGTTTCTGTAACAAATGAGC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 erLeuLeuAspProAspGlnAspAlaThrTyrPheGlyAlaPheLysVal 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 ePheLysLeuArgAlaGlyGluGluIleSerIleGlnValSerAsnProS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="IMAGE:1697383"
/clone_llb="Soares_pregnant_uterus_NbHPU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 TyrLeuTyrAlaAsnIleCysPheArg...HisHisGluThrSerGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 rValProThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 leLysIleProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 36.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
                            GI:3434829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
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TITLE
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ORIGIN
                                                                              SOURCE
                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adenocarcinoma"
/lab.host="DH10B"
//note="Organ: pencreas; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned undirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI095853 468 bp mRNA EST 05-OCT-1998 qb2604.x1 Seares_preparat_uterus_NbHpU Homo sapiens cDNA clone IMAGE:1697383 3' similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING LIGAND; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 TTGAGGAATGGTGAACTGGTCATCCATGAAAAGGGTT TACTACATCTA 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 | TICCCAAACATACTITCGATTTCAGGAGGAAATAAAAGAAAACCAAAGAC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 IleAsnValGlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIl 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               290 eGlnValSerAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230 TTCTGTAACAATGAGCACTTGATAGACATGGACCATGAAGCCAGTTTT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 rValValLysThrSerIleLysIleProSerSerHisAsnLeuMetLysG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T......CCTGACCCTATATTGTTGATGAAAA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200.LeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 GACAAACAAATGGTCCAATA.....TATTTACAAATACACAGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 lyGlySerThrLysAsnTrpSerGlyAsnSerGluPheHisPheTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 111111::||||:::|||:::||| ::
280 ATCTATCAAGGGGGAATTTTGAGCTTAAGGAAAATGACAGAATTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....ThrSerGlySerValProThrAspTyrLeuGlnLeu.MetValTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 35.772
                                                                                                                          Possible reversed clone: polyT not found Seq primer: -400P from Gibco High quality sequence stop: 383.

Location/Qualifiers
                                                                           www-bio.llnl.gov/bbrp/image/image.html
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/clone_lib="NCI_CGAP_Pan1"
                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                               /db_xref="taxon:9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 TIGGGGCCTTTTAGTT 164
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Ratio:
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BASE COUNT

FEATURES

to: 468

356

DEFINITION

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183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe
                                                                                                                                                                                                                                                                                                                                                                                                                                           seg_name: qb_est11:A1626285
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LOCUS A1626285
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                            AA298009 320 bp mRNA EST 18-APR-1997 EST113646 T-cell lymphoma Homo sapiens cDNA 5' end similar to Apo-2 Ligand (tumor necrosis factor), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995) 96026280
                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site_1: EcoRI; Site_2:
224 ACTTGATAGACATGGACCATGAAGCCAGTTTTTTCGGGGCCTTTTTAGTT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850
Tel: 3018699056
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Identity: 34.314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="ATCC (inhost):165358"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-;
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_ESTs: THC183094
Contact: Kerlavage, AR
                                                                                                                                     AA298009
AA298009.1 GI:1950414
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                                           seq_name: gb_est3:AA298009
                                                                         Quality:
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                                                                                                                                                                                       human.
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SOURCE
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Actinopterygii; Neopterygii; Teleostei; Euteleostemi; Satariophysi; Cyprindformes; Cyprinidae; Rasborinae; Danio.

Cypriniformes; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 218)

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hiller,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,W., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Kohnler,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI626285 218 bp mRNA EST 23-APR-1999 fc12f06.yl Zebrafish WashU MPIMG EST Danio rerio CDNA 5' similar to SW:TRAL_MOUSE P50592 TNF-RELATED APOPTOSIS INDUCING LIGAND ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@qenomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumprimarbatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tal: 314 286 1800
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 TCCTGACCCTATATTGTTGATGAAAGTGCTAGAAATAGTTGTTGGTCTA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand Seq primer: T3 ET from Amersham High quality sequence stop: 113.
Location/Qualifiers
                                                                                                                             113 TCTATTCCCAAACATACTTTCGATTTCAGGAGGAAATAAAAGAAAACACA 162
                                                                                                                                                                                                                                                                                                                                                                                                         232 ThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysIl 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 eProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 AAGATGCAGAATATGGACTCTATTCCATCTATCAAGGGGGATATTGAGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 AAGAACGACAAACAAATGGTCCAATATTTTNCAAATACACA...AGTTA
13 ATAAACTCCTGGGAATCATCAAGGAGTGGGCATTCATTCCTGAGCAACTT
                                                                               198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrL
                                                                                                                                                                                                                                                  215 euTyrAlaAsnIleCysPheArgHisHisGluThrSerGlySerValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:7955"
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A1626285.1 GI:4663085
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source
                                           JOURNAL
MEDLINE
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                              //doc="Vector: pSport1; Site_1: Not1; Site_2: Sal1; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer |

//ord="Vector: pSport1; Site_1: Not I - oligo(dT)15 primer |

//ord=Tranded cDNA was ligated to Sal I adaptors (BRL),

double-stranded cDNA was ligated to Sal I adaptors (BRL),

digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; LORG) and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryotza: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 675)
1 (bases 2 to 675)
1 (bases 3 to 675)
1 (bases 4 to 675)
1 (bases 4 to 675)
1 (bases 6 to 675)
1 (bases 6 to 675)
2 (bases 7 to 675)
2
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MRO-BN0070-200400-015-e10 BN0070 Homo sapiens CDNA, mRNA sequence.
BE000089
                                                                                      /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86| CGCAGAATACGCCCTGCACTGGGTGTACCAGGGCGGCCTGTTCGAGCTCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283 rgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAsp 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 GAGCAGGCGATGAGGTCTTCGTGTCCGTCTCATCTCCCACAATGGTCTAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 nSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuA
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 40.984
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 ProAspGlnAspAlaThrTyrPheGlyAlaPhe 310
                                                                                                                                                                                 /lab_host="XL1-blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE000089.1 GI:8260322
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1 67 c
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83.607
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US-08-989-362-2 x AI626285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est32:BE000089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS BE000089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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VERSION
KEYWORDS
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/dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: breast_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MRO-BN0070-200 Seq primer: puc 18 forward
                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 gLeuHisGluAsnAlaGlyLeuGlnAspSerThrLeuGluSerGluAspT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 TTAAAAGAAGATGACAGTTATTGGGAC.....CTCTATGACGAAGAGA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655 CGCCGCTGCTTGGCTGACTACAGCAGTCAGCTCTGACAGGATCATGTCTA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 ..... 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 gSerSerGluGluMetGlySerGlyProGly.....ValProHisGluG 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 lyProLeuHisProAlaProSerAlaProAlaProAlaProProProAla 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 AlaSerArgSerMetPheLeuAlaLeuLeuGlyLeuGlyLeuGlyGlnVa 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 lValCysSerIleAlaLeu...PheLeuTyrPheArgAlaGlnMetAspP 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 roAsnArgIle.SerGluAspSerThrHisCysPheTyrArgIleLeuAr 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      555 GTGATCTTCACAGTGCTCCTGCAGTCTCT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 243
Gaps: 12
Percent Identity: 24.691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
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156 g 202 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BN0070"
                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 63
High quality sequence stop: 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .675
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                                                                                                                                                                                   Tel: +55-11-2704922
Fax: +55-11-2707001
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49.383
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  Proc. Nat
20202663
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                                                                                                                                                                Brazil
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11	<pre>0 hrLeuProAspSerCysArgArgMetLysGlnAlaPheGlnGlyAlaVal</pre>	126
39	::::: :::: :::::	349
127		143
348	8 AGAAAGAAAGCAACAAAATATTCTCCCCTA	317
14	3 oAlaMetMetGluGlySerTrpLeuAspValAlaGlnArgGlyLysProG	160
31	316GTGAGAGAAAGGGTCCTCAGA 295	295
16	0 luAlaGinProPheAlaHisLeuThrIleAsnAla	171
29	594 GAGTAGCAGCTCACATAACTGGGACCAGAGGAAGAAGCAACAA 251	251
17	2 AlaSerIleProSerGlySerHisLysValThrLeuse	184
25	250 TTGTCTTCTCCAAACTCCAAGAATGAAAAGGCTCTGGGCCGCAAAATAAA	201
184		200
200	: ::: ::: :::	151
200		216
150	0 TGAGGAATGGTGAACTGGTCCATGAAAAAGGGTTTTACTACATCTAT	101
217	7 AlaAsnIleCysPheArgHisHisGlu 225	
100	:::::: ::: 0 TCCCATACATACTTTCAGGAG 74	